

FIGURE 1

CGGACGCGTGGGTGCGAGGCGAAGGTGACCGGGGACCGAGCATTTTCAGATCTGCTCGGTAGAG
 CCTGGTGCACCACCACCATGTTGGCTGCAAGGCTGGTGTGTCTCCGGACACTACCTTCTAGG
 GTTTTCCACCCAGCTTTCCACCAAGGCCCTCCCTGTTGTGAAGAATTCATCACGAAGAATCA
 ATGGCTGTTAACACCTTAGCAGGGAATATGCCACCAAAACAAGAATTTGGGATCCGGCGTGGGA
 GAACTGGCCAAGAAGCTCAAAGAGGCAGCATTGGAACCATCGATGGAAAAAATATTTAAATTT
 GATCAGATGGGAAGATGGTTTGTGTCTGGAGGGGCTGCTGTTGGTCTTGGAGCATTTGTGCTA
 CTATGGCTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAAATTTGGCCCTCAGT
 ATGTCAAGGATAGAATTCATTCCACCTATATGTACTTAGCAGGGAGTATTGGTTTAAACAGCT
 TTGTCTGCCATAGCAATCAGCAGAACGCCCTGTTCTCATGAACCTCATGATGAGAGGCTCTTG
 GGTGACAATTTGGTGTGACCTTTGCAGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATAC
 CATATGACCAGAGCCAGGCCCAAAGCATCTTGCTTGGTTGTACATTCCTGGTGTGATGGGT
 GCAGTGGTGGCTCCTCTGACAATATTAGGGGGTCCCTCTTCTCATCAGAGCTGCATGGTACAC
 AGCTGGCATTGTGGGAGGCCCTCTCCACTGTGGCCATGTGTGCGCCAGTGAAGAGTTTCTGA
 ACATGGGTGCACCCCTGGGAGTGGGCCCTGGGTCTCGTCTTTGTGTCTCATTTGGGATCTATG
 TTTCTTCCACCTACCACCGTGGCTGGTGGCCACTCTTTACTCAGTGGCAATGTACGGTGGAT
 AGTTCTTTTCAGCATGTTCTTCTGTATGATACCCAGAAAGTAATCAAGCGTGCAGAAGTAT
 CACCAATGTATGGAGTTCAAAAATATGATCCCATTAACTCGATGCTGAGTATCTACATGGAT
 ACATTAATATATATTTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCCAACAGAAAGAAATG
 AAGTGACTCAGCTTCTGGCTTCTCTGCTACATCAAATATCTTGTTTAATGGGGCAGATATGC
 ATTTAAATAGTTTGTACAAGCAGCTTCGTGTAAGTTTAGAAGATAAGAAACATGTCATCATA
 TTTAAATGTTCCGGTAATGTGATGCCTCAGGTCTGCCTTTTTTTCTGGAGAATAAATGCAGT
 AATCCTCTCCCAAATAAGCACACATTTTCAATCTCATGTTTGGAGTGATTTTAAATGT
 TTGGTGAATGTGAAAACATAAGTTTGTGTATGAGAATGTAAGTCTTTTTTCTACTTTAAAA
 TTTAGTAGGTTCACTGAGTAACTAAATTTAGCAAACCTGTGTTGCATATTTTTTTGGAGT
 GCAGAATATTGTAATTAATGTCATAAGTGATTTGGAGCTTTGGTAAAGGGACCAGAGAGAAG
 GAGTCACCTGCAGTCTTTTGTTTTTTAAATACTTAGAACTTAGCACTTGTGTTATTGATTA
 GTGAGGAGCCAGTAAGAAACATCTGGGTATTGGAACAAGTGGTCATTGTTACATTCATTT
 GCTGAACTTAACAAAACCTGTTTCATCCTGAAACAGGCACAGGTGATCATCTCCTGCTGTTG
 CTTCTCAGTGCTCTTTTCCAATATAGATGTGGTCATGTTTGAAGTGTACAGAAATGTTAATC
 ATACAGAGAATCCTTGATGGAATTATATATGTGTGTTTACTTTTGAATGTTACAAAAGGAA
 ATAACCTTTAAACTATTCTCAAGAGAAAATATTCAAAGCATGAAATATGTTGCTTTTTCCAG
 AATACAAACAGTATACTCATG

FIGURE 2

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRTGQEL
KEAALEPSMEKIFKIDQMGRWFVAGGAAVGLGALCYYGGLSNEIGAIEKAVIWPQYVKDRI
HSTYMYLAGSIGLTALSAIAISRTPVLNFMFMRGSSWVTIGVTFAMVGAGMLVRSIPYDQSP
GPKHLAWLLHSGVMGAVVAFLTILGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL
GVGLGLVFVSSLGSMFLPPTTVAGATLYSVAMYGGLVLFMSMFLLYDTQKVIKRAEVSPMYGV
QKYDPINSMLSIYMDTLNIFMRVATMLATGGNRKK

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FIGURE 3

GAAGGCTGCGCTCGCTGGTCCGAATTGCGGTGGCGGCACGTCGCCCGCTCTCCGCCCTTCTGCAT
 CGCGGCTTCGGCGGCTTCCACCTAGACACCTAACAGTCGCGGAGCGCGCGCGTCTGAGGG
 GGTTCGGCAGCGGGAGTTCGGGCGGCTCTTGTCATCTTGGCTACCTGTGGGTTCGAAGATGTCGG
 ACATCGGAGACTGGTTCAGGAGCATCCGCGCATCACGCGCTATTGGTTCGCCGCGCACCGTTC
 CGCGTGCCTTGGTTCGGCAAACTCGGCCCTCATCAGCCCGGCCCTACCTCTTCTCTCGGCCGGA
 AGCCTTCCTTTATCGCTTTCAGATTTGGAGGCCAATCAGTCCACCTTTTATTTCCCTGTGG
 GTCCAGGAATCTGGATTTCTTTATTTGGTCAATTTATATTTCTTATATCAGTATTCTACGCGA
 CTGTAACACAGGAGCTTTTGATGGGAGGCCAGCAGACTATTTATTCGCTCTCTTTAACTG
 GATTTGCATCTGATTTACTGGCTTAGCAATGGATATGCACTGCTGATGATTTCTCTGATCA
 GTTCAGTATTTATGCTGGGCCAGCTGAACAGAGACATGATTTGATATCATTTGGGTTTGA
 ACAGATTTTAAAGCTGCTATTTACCTGGGTATCCTTGGATTCACATATATCATCGGAGG
 CTGGTAAATCAATGAGCTTTTGGAAATCTGGTTGACATCTTTATTTTCTCAATGTTCA
 GATACCAATGGAGCTGGGAGGAAGAAATTTCTATCCACCTCAGTCTTTTGTAGACCGCTGG
 CTGCCAGTAGGAGAGGAGGACTATCAGGATTTGGTGTGCCCTGCTAGCATAGGCGAGC
 TGTGATCAGAATGGCGAGGCGGAGACACAACCTGGGCGCAGGGCTTTCGACTTGGAGAGC
 AGTGA
 AGTGAAGGCGGCTCGGCGAGCGGCTCTCAAGCCACATTTCTCCCGAGTGTGGGG
 CACTTAACAACTCGCTTCGGCTAACACTGTGGAGCTGACCACACTGAATGTAGTCTTTC
 AGTACGAGCAAACTTCTTAAATCCCGAAGAAATATAAGTGTCCACAACTTTCAGGAT
 TCTCAATTCAGTCTTACTGCTGTGAAGACAAATACCACTGTGCAAAATGCAAACTGAC
 TACATTTTGGTCTCTCTCTTCTCCCTTTCCGCTCAATATGGGTTTAGCGGCTCT
 AATCTGCTGTCATTTAGCTGGGGCTGGGTACCAAAACCTTCCAAAGAGACCTTATCTCTT
 TCTTGACACATGCTCTCTCCACTTTTCCAAACCCACATTTGCAACTAGGAAAAGTTG
 CCCATAAAATTTGCTCTGCCCTTGACAGGTTCTGTTATTTATTGACTTTTGCAAGGCTGGT
 ACACAACATCATATTCAGGTTATTTTCCCTTTTGGTGGCAGAAGTCTTACCAATGAGGGGAG
 AAGACAGCCACGGATGAAGCGTTTCTCAGCTTTTGGAAATGCTTCGATGACATCCGTTGGT
 AACCGTTTGGCACTCTTCAGATATTTTTATAAAAAAGTACCACTGAGTTTCATGAGGGGCA
 CAGATTTGGTTATTAATGAGATACGAGGGTGGTGTGGTGTGTTTCTGAGCTAGCTGA
 TCAAGACTGTAGTGGAGTTGCACTAACATGGGTAGGTTTAAACCATGGGGGATGACACCC
 TTTGCGTTTCATATGTAGCCCTACTGGCTTTGTGTAGCTGGAGTTTGGTGTGTTGTGT
 TAGGAGGATCCAGATCATGTTGGCTACAGGGAGATGCTCTCTTTGAGAGGTCCTGGGCATTG
 ATTCCCATTTCAATCTCATTCTGGATATGTGTTTCATTGAGTAAAGGAGGAGAGACCCCAT
 CGCTATTTAAATGTCATTTTTTGCTATCCCCCGTTTTTGGTTCATGTTTCAATTAATTTG
 GAGGAAGGCGCAGCTCCTCTCTGCACGTAGATCATTTTTTAAAGCTAATGTAAGCACATCT
 AGGGAATAACATGATTTAAGGTGAAATGGCTTTAGAATCATTTTGGTGTGAGGGTGTGTTA
 TTTTGTGTCATGAATGTACAAGCTCTGTGAATCAGACCACTTAAATACCCACACCTTTTT
 TCGTAGGTGGGCTTTTCTATCAGAGCTTGGCTCATAAACCAATAAGTTTTTTGAAGGCCA
 TGCGTTTTACACAGTTATTTTATTTATGACGTTATCTGAAAGCAGACTGTTAGGAGCAGT
 ATTGAGTGGCTGTCACTTTTGAAGCACTAAAAAGGCTTCAACAGTTTGTATCAGTTTCTT
 TCCAGGAACATTTGTCTTACAGTATGACTATTCTTTCCCCACTCTTAAACAGTGTGAT
 GTGTGTTTACCTAGGAATGAGAGTTGGCAACAACTTCTCATTTTGAATAGAGTTTGTGTG
 TACTTCTCCATTTTAAATTTATATGATAAAATAGGTGGGAGAGCTGGAACCTTAACTGCA
 TGTTTTGTGTTTCATCTGTGGCCCAATAAAGTTTACTTGTAAAAATTTAGAGGCCATTA
 CCAATATTTGACGTCACACTCATTTGTACAGCGCTGGAGACTTGTGATGTATAAGAAATA
 TTTCTGACAGTGTGAGTGACCGGAGTCTCTGTGTGACCTCTTACCAGTCAGCTGCGTGGAG
 CAGTCAATTTTCTTCAAGGTTTACAAGTATTTAGAATTTTGAATTTGCTGAGGCAAAATGTT
 ATGAACTTATTTCTCTTAAACATGTTTAGGAAGCTGATGACGTTTATTTGATTTGTCTGGATT
 ATGTTTCTCGGAATAATTTTACCAAAACAGCTATTTGATTTTGAATTTGACTTGACAAGGCAAA
 TGACATGGATTTCTCTTTACAATGGAAAAAAATCTTATTTTGTATTAAGGACTTCCC
 TTTTGTGAATAATCTCTTTTATTTGGTAAAAATTTGAATAATAAATGTCACATTTG

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FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLG LISPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFLYLVNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWGQGFRL
GDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

FIGURE 5

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTTGCATTAACTGGTTG
 GTAGCTTCTATCCTGGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCCTACTCCCTCTCGGCT
 CCTTGTGGCCCAAAGGCCATAACGGGGTCCGGCGGTCTGGCCTAGGGATCTTCCCCGTTGCC
 CCTTTGGGCGGG**CATGG**GCTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATCG
 CGGGGTTCTGCGAGGCCAGACTGGTCCATCCCCATCTTGGACTTTGTGGAACAGAAATGT
 GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCCAGAGCCGGTGATTTTGGT
 GGCCTGTGTTCCCTTGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTC
 ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTAGAAGGTTACCTCAAAGAAATTGGAATT
 AATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAGGC
 CATTTTGCAACCTGTGTTGGCAGCAGAAGATTTACTATCTTTAAAGCAATGATGGTCCAGA
 AAAACATTGAAATGCAGCTGCAAGCCATTGCAATAATTCAAGAGAGAAATGGTGTATTACCT
 GACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAAACAGCAAGAGATGAAAATCCT
 GAGGGAAGTTCTTAGAAAAATCAAAAGAGGAATATGACCAGGAAGAAGAAAGGAGAGAAAA
 AACAGTTATCAGAGGCTAAAAACAGAAGAGCCCACAGTGCATTCCAGTGAAGTGCAATAATG
 AATAATTCCCAAGGGATGGTGAACATTTTGCACACCCACCTCAGAAGTTAAATGCATTT
 TGCTAATCAGTCAATAGAACCTTTGGGAAGAAAAGTGAAGGTCTGAAACTTCTCCCTCC
 CACAAAAAGGCGCTGAAGATTCCTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAA
 TTATCAGTACTTGAACAGAGAAGAACTTCGGCAACGAGAACACTATCTCAAGCAGAAGAGAGA
 TAAGTTGATGTCCATGAGAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG
 GAAAACCCACTGGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAAG
 CAAACATTACTAAAGAGGAGATTGCTTGAGAGAAACTCAAAGAAGAAGTTATTAATAAG**TA**
ATAATTAAGAACAATTTAACAAAATGGAAGTCAAATTGTCTTAAAAATAAATTATTTAGTC
 CTTACACTG

FIGURE 6

MAAEEDEVEWVVESTIAGFLRGPDWSIPILDFVEQKCEVNCCKGGHVITPGSPPEPVILVACVP
LVFDDEESKLTYTEIHQEYKELVEKLLEGYLKEIGINEDQFQEACTIONPLAKTHTSQAILQP
VLAAEDFTIFKAMMVQKNIEMLQAIIRIIQERNGLVLPDCLTDGSDVVSLEHEEMKILREVL
RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPIANLSVLGTEELRQREHYLKQKRDKLMS
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEEKQTLLKRLLAEKLEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

GGGCACAGCACATGTGAAGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT
TCATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGTTACCTCAAAGAAATTGGAA
TTAATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCATACATCACAG
GCCATTTTGGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC
AGAAAAGCAATGAAATGCAGCTGCAAGCCATTGCAATAATTCAGAGAGAAATGGTGTATTA
CCTGACTGCTTACCAGTAGGGCTCTGATGTGGTCACTGACCTTGAACACGAAGAGATGAAAT
CCTGAGGGAAGTCTTTAGAAAATCAAAGAGGAAATGATGACCAGGAA

FIGURE 8

GCGTGGTTTTTGTCTGCAATAGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTG
 TAGCTTCTCCACGTATGGACCTTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTG
 TCTCAGCTCTAGGATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAACAAAC
 AGTGGAAATGGAAAAACAGTGTGTAGTCACTCGTAATATGCTCCTTGTCAACAATGTATAC
 ATTCCCTGCTAGGTGCCATATTCTTCTTAAAGCTCAAGTCGCATCTTACTAGTGAAGTATT
 CTGCCAATGAAGAAAAACAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAACTG
 GTGAAGCTAGTTTTCTGTGCTTGTGTCATCTGTGTATAAAGAAAGATCATCAAAGTAG
 AAATTTGAATATGCTTCTCGGAAGGAATCTCTGATTTCATGAAGTGGTCCATTCTCGCCT
 TTCTTTATTTCTGGATAACTTGATGTCTTCTATGTCCTGTCTTCTCAACCAGCCATG
 GCTGTTATCTTCTCAAATTTTAGCATTATAACAACAGCTCTTCTATTCCAGGATAGTGCTGAA
 GAGGCGTCTAACTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCT
 TGACTGCCGGGACTAAAACCTTACAGCACAACTTGGCAGGACGTGGATTTCATCACGATGCC
 TTTTTCAGCCCTTCCAATTCTCGCCTTCTTTTCAAGAGTGAAGTGTCCAGAAAAGACAATTG
 TACAGCAAAGGAATGGACTTTTCTGAAGCTAAATGGAACACCACAGCCAGAGTTTTCAGTC
 ACATCCGTCTTGGCATGGGCCATGTTCTTATTATAGTCCAGTGTTTTTATTCTTCAATGGCT
 AATATCTATAATGAAGAAGATACTGAAGGAGGGGAACAGCTCACTGAAGACATCTTCATACA
 GAACAGCAACTCTATTCTTTGGCATCTGTTAATGGGCTGACTCTGGGCGCTCAGAGGA
 GTAACCGTGATCAGATTAAAGAACTGTGGATTTTTTATGGCCACAGTGCATTTTCAGTAGCC
 CTTATTTTGAAGTGCATTCAGGGGCTTTCAGTGGCTTTCATTCTGAAGTTCCTGGATAA
 CATGTTCCATGCTTGTGATGGCCAGGTTACCAGTGCATTATACACAAGTGTCTGTCTCTGG
 TCTTTGACTTTCAGGCCCTCCCTGGAATTTTTCTTGAAGCCCCATCAGTCTTCTCTCTATA
 TTTATTATAATGCCAGCAAGCCTCAAGTTCGGGAATACGCACCTAGGCAAGAAAGGATCCG
 AGATCTAAGTGGCAATCTTTGGGAGCGTTCCAGTGGGGATGGAGAAGAACTAGAAGACTTA
 CCAAACCCAAAGATGATGAGTCAGATGAAGATACTTCTTAACTGGTACCCACATAGTTTGCA
 GCTCTCTTGAACCTTATTTTACATTTTTCAGTGTGTTGTAATATTATCTTTTCACTTTGATA
 AACCAGAAATGTTTCTAAATCCTAATATTCTTTCATATATCTAGCTACTCCCTAAATGGTT
 CCATCCAAGGCTTAGAGTACCCAAGGCTAAGAAATTTCTAAAGAACTGATACAGGAGTAACA
 ATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATATGTGCAGATTAT
 TTTCTCTGGCCTTCAAGCTTCCAAAAAAGTGTGAATAATCATGTTAGCTATAGCTTGTATAT
 ACACATAGAGATCAATTTGCCAAATATTCACAATCATGTAGTTCTAGTTTACATGCCAAAGT
 CTTCCCTTTTTAACATTATAAAAGCTAGGTGTCTCTTGAATTTGAGGCCCTAGAGATAGT
 CATTTTGCAGTAAAGAGCAACGGGACCTTCTTAAAAACGTTGGTTGAGGAGAAAAATCTGTG
 CTGGCCATACCATAGATTTTGGGATGATGAGTCTGTGCTAAATATTTTGTGGAAGAGCACT
 TTCTCAGACACAACATCTCAGAATTTTAATTTTTAGAAATTCATGGGAAATTTGATTTTTGT
 AATAATCTTTTGATGTTTTAAACATTGGTTCCTCTAGTCAACATAGTTACCCTTGTATTTTA
 AGTCATTTAAACAAGCCACGGTGGGGCTTTTTCTCCTCAGTTTGAAGGAGAAAAATCTGTG
 GTCATTACTCTGAAATTATTACATTTTGGAGAAATAAGAGGGCATTTTATTTTATTAGTTACT
 AATTCAAGCTGTGACTATTGTATATCTTTCCAAGAGTTGAAATGCTGGCTTCAGAATCATAC
 CAGATTGTCAAGTGAAGTGTGCTTAGGAACCTTTAAAGGGATCCTTTCAAAGGATCACTT
 AGCAACACATGTTGACTTTTAACTGATGTATGAATATTAATACTCTAAAAATGAAGAGCC
 AGTAATATATAAGTCACTTTTACAGTGTCTTACACTTCAACACTTAAAGTGATGTTATTTGATG
 GTATTTTGATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTA
 AAATTCAGCAACAAAAGTGACTTGCTCAGGGTCAATGTCAGCTGGGTGATGATGAAGAGTGGG
 CTTTAACTGGCAGGCTGTATGTTTACAGACTACCATACTGTAATATGAGCTTATGCTGTG
 CATTTCTCAGAACTTATACATTTCTGCTCTCTTTCTCCTAAGTTTCATGCAGATGAATATA
 AGGTAATATACTATTATATAATTCATTGTGATATCCCAATAATATGACTGGCAAGAATTG
 GTGGAAATTTGTAATAAAAATAATTATTAACCTT

MEKQCCSHPVICLSLSIMYTFLLGAIFIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
LVFVCLVSPFCVIKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLQPAMAV
IFSNFSIITTALLFRIVLKRRLNWIQWASLLTFLSIVALTAGTKTLQHNLAGRGFHHDAFF
SPSNSCLLFRSECPRKDNCTAKEWTFPEAKWNNTARVFSHIRLGMGHVLIIVQCFISSMANI
NEKILKEGNQLTESIFIQNSKLIFYGGLFNGLTGLQRSNRDQIKNCGFFEYGHSAFSAI
VYTAQGLSVAFILFLDNMFHVLMAQVTTVIITTVSLVDFRPSLEDFLEAPSVLLSIFI
YNASKPOVPEYAPRQERIRDLSGNLWERSGDEGELERLTKPKSDESDETF

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
298-318, 328-368

amino acids 128-132, 204-208, 218-222, 374-378

amino acids 402-406

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

FIGURE 10

CGTGCCTGCGCAATGGGTGTCGGGTCCGCTTTTCCCAATCCGGACGTAATCGTGGTTTTTG
TTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCAC
GTATGGACCCATAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAACAAACAGTGGAATGGAA
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCACAATGTATACATTCCTGCTAGG
TGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG
AAAACAAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA
TGCTTCCTGGAAGGAATTCTCTGATTTTCATGAAGTGGTCCATTCTGCCTTTCTTTATTTCC
TGGATAACTTGATTGTCTTCTATGTCCTGTCCATCTTCAACCAGCCATGGCTGTTATCTTC
TCAAATTTTAGCATTATAACAACAGCTCTTCTATTACAGGATAGTGCTGAAGAGGCGTCTAAA
CTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCTTGACTGCCGGGA
CTAAAACTTTA

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FIGURE 11

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGGCCGGCTTGCTAGCGCGCGGGCC
 GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCCCTGCGGGGCGAGGAGCAT
 CCCGCTTACCAGGTTCCCAAGCGGCGTGGCCCGCGGGTCATGGCCAAAGGAGAAGGCGCCGAG
 AGCGGCTCCGCGCGGGGCTGCTACCCACCAGCATCCTCCAAAGCACTGAACGCCCGGCCCA
 GGTGAAGAAAGAACCGAAAAAGAAACACAGTTGTCTGTTTGAACAAGCTTTGCTATG
 CACTTGGGGAGCCCCCTACCAGGTGACGGGCTGTGCCCTGGGTTTCTTCCCTCAGATCTAC
 CTATTGG^{ATGT}GGGCTCAGGTGGGCCCTTTCTCTGCCTCCATCATCTGTTTGTGGGCCGAGC
 CTGGGATGCCATCACAGACCCCTGGTGGGCTCTGCATCAGCAATCCCCCTGGACCTGCC
 TGGGTCGCTTATGCCCTGGATCATTTCTCCACGCCCTGGCCGTATTGCTACTTCCCTC
 ATCTGGTTCGTGCCGACTTCCACACGGCCAGACCTATTGGTACCTGCTTTCTATTGCTT
 CTTTGAACAATGGTCACGTGTTTCCATGTTCCCTACTCGGCTCTCACCATGTTTCATCAGCA
 ACCGAGCAGACTGAGCGGGATTCTGCCACCGCCTATCGGATGACTGTGGAAGTGCTGGGCAC
 AGTGCTGGGCACGGCGATCCAGGGACAAATCGTGGGCCAAGCAGACACGCCCTTGTTCAGG
 ACTTCAATAGCTCTACAGTAGCTTCAAAAAGTGCCAAACCATACATGGCACCACCTTCACAC
 AGGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGCTCATTTGCTGTATCTATATAATCTG
 TGCTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCAGCAGTCTG
 AGCCAAATCGCTACTTCCGGGGCTACGGCTGGTCATGAGCCACGGCCATACATCAAATTT
 ATTACTGGCTTCCCTTTCACCTCCTTGGCTTTTCATGCTGGTGGAGGGGAACCTTGTCTTGT
 TTGCACCTACACCTTGGGCTTCCGCAATGAATTCAGAATCTACTCCTGGCCATCATGCTCT
 CGGCCACTTTAAACCATCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCT
 GTATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAA
 CCTCATCATTACATATCGGCTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTAC
 TACCTGGTCCATGCTGCCTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCAT
 GGAACCGAGCCCATCTTCTTCTCCTTCTATGTCTTTCACCAAGTTTGCCTCTGGAGTGTC
 ACTGGGCATTTTACCTCAGTCTGGACTTTGCAGGATACCAGACCCGCTGGCTGCTCGCAGC
 CGGAACGTGTCAAGTTTACACTGAACATGCTCGTGACCATGGCTCCCATAGTTCTCATCCTG
 CTGGGCGCTGCTGCTTTCAAAATGTACCCCATTGATGAGGAGAGGCGCGGCGAGAATAAGAA
 GGCCCTGCAGGCACTGAGGGACGAGGCCAGCAGCTCTGGCTGCTCAGAAACAGACTCCACAG
 AGCTGGCTAGCATCCTCTAGGGCCCGCCACGTTGCCCGAAGCCACCATTGCAGAAGGCCACAG
 AAGGATCAGGACTGTCTGCCGCTTGTGAGCAGCTGGACTGCAGGTGCTAGGAAGGGAA
 CTGAAGACTCAAGGAGGTGGCCAGGACACTTGTGTGCTCACTGTGGGGCCGGCTGCTGT
 TGGCTCTGCTCCTCCCTCTGCCTGCCTGTGGGGCCAAAGCCCTGGGCTGCCACTGTGAATA
 TGCCAAGGACTGATCGGCGCTAGCCCGGAACATAATGTAGAAACCTTTTTTTTACAGAGCC
 TAATTAATAACTTAATGACTGTGATACATAGCAATGTGTGTGTATGTATGTCTGTGAGCTA
 TTAATGTTATTAATTTTCATAAAAGCTGGAAGC

MWLRWALSLPSSCLWAEFGMPSQTPWWASANPPGPAWVALCPGSSSPRPWPSLPTSSSG
SCPTSHRTARPIGTCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL
GTAIQGQIVGQADTPCFQDFNSSTVASQSANHTGTTSHRETQKAYLLAAGVIVCIYIICAV
ILILGVREQREPYEAQQSEPIAYFRGLRLVMSHGPHYIKLITGFLTSLAFMLVEGNFVLFT
YTLGRNEFQNLLAIMLSATLTIPIQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLI
ITYAVAVAAGISVAAFFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLG
ITSLDLDFAGYQTRGCSQPERVKFTLNLMLVTMAPIVLILLGLLLFKMYPIDEERRQNKKAL
QALRDEASSSGCSESTFASLIL

GGGAAACGCAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTGT
GCTGTCATCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCATGAAGCCCAGCAGTCTGA
GCCAATCGCCTACTTCCGGGGCTACGGCTGGTCATGAGCCACGGCCATACATCAAACCTTA
TTACTGGCTTCCTCTTCACTTCTTGGCTTTCATGCTGGTGGAGGGGAACCTTGTCTTGT
TGCACCTACACCTTGGGCTTCCGCAATGAATTCAGAATCTACTCTTGGCCATCATGCTCTC
GGCCACTTTAAACCATTCCTGTCAGTGGTCTTGGACCCGGTTTGGCAAGAAGACAGCTG
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC
CTCATCATTACATATCGGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT
ACCTTGGTCCATGCTGCTGATGTCAATTGACGACTCCATCTGAAGCAGCCCCACTTCCATG
GAACCGAGCCCAT

FIGURE 14

GGGGCTTCGGCGCCAGCGCCAGCGCTAGTCGGTCTGGTAAGGATTACAAAAGGTGCAGGT
ATGAGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAAACAGAAAACCTGTTAGAAAATGT
GGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT
TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT
CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG
CAGTTTTATGCATTGCTACCATTTATGTTTCGTTATAAGCAAGTTTCATGCTCTGAGTCCTGAA
GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGTAAGTGGAACTAGAGTTGTTTAGG
ACTTTCTATTGTGGCAAACCTCCAGAAAACAACCCCTTTTGTGTCACATGTAAGTGGAGCTG
TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTCAGACCATCCTTTCTACCAAATG
CAGCCCAAATCCATGGCAAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG
AGTAAGTGCACCTTAGCATGCTGACTTGCTCATCAGTTTTGCACAGTGGCAATTTTGGGACTG
ATTTAGAACAGAAAACCTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACT
ACTGCAGCAGAAATGGTCTATGTCATTTTCCTTCTTTGGTTTTTCTGACTTACATTCTGTGA
TTTTTCAGAAAATTTCTTTACGGGTGGAAGCCAAATTTACATGGATTAAACCCTCTATGACACTG
CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCAGAGATATTTGATGAAAGGAT
AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGGTTACAGAAGTTGCTTA
TTCTTCTCTGAAATTTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
ATCAGGAAACATGAAAGAAGCCATTTGATAGATTATCTAAAGGATATCATCAAGAAGACTA
TTAAAAACACCTATGCCTATACTTTTTTATCTCAGAAAAATAAGTCAAAAGACTATG

FIGURE 15

MWWFQQGLSFLPSALVIWTSAAFIJSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI
AAVLCIATIIYVRKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSG
AVLTFGMGSLYMFVQTIILSYQMOPKIHGKQVFWIRLLVIWCGVSALSMLTCSSVLHSGNFG
TDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFLTYIRDFAQISLRVEANLHGLTLYD
TAPCPINNERTRLRSRDI

099999.111903

FIGURE 16

CGGACGCTTGGGCNCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT
TCCGTCTCTCGGGTCTTTTCCCTGGTCCCAGGCCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAATTCCTCTGGTTTGTGAAGCAGT
TACCAAGAATCTTCAACCCTTTCCCAAAAAGCTAATTGAGTACACGTCCTGTTGAGTACA
CGTTCCTGTTGATTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA
GTTGTAAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCT
TCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACT
CCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

FIGURE 17

CCCACGCGTCCGCCCGCGCTGCGTCCCGGAGTGCAAGTGAGCTTCTCGGCTGCCCCGCGGG
 CCGGGTGCGGAGCCGACATGCGCCGCTTCTCGGCTCCTTCTGGTCTTCGCCGGCTGCAC
 CTTGCGCTTGTACTTGTGTGACGCGACTGCCCGCGGGCGGAGACTGGGCTCCACCGAGG
 AGGCTGGAGGCAGGTGCTGTGGTTCCCTCCGACCTGGCAGAGCTGCGGGAGCTCTCTGAG
 GTCCTTCGAGAGTACCGGAAGGAGCACCAGGCCTACGTGTTCTCTGCTCTTCTGCGGCGCCTA
 CCTCTACAAACAGGGCTTTGCCATCCCCGGCTCCAGCTTCTGAATGTTTTAGCTGGTGCCT
 TGTTTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTTGACCTCGGTGGGTGCCACATGC
 TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCTGATAAAGT
 GGCCCTGCTGCAGAGAAAGGTGGAGGAGAACAGAAACAGCTTGTTTTTTTCTATTGTTTT
 TGAGACTTTTCCCATGACACCAAAGTGGTTCTTGAACCTCTCGGCCCAATTCTGAACATT
 CCCATCGTGCACTTCTTCTCTCAGTTCTTATCGGTTTGATCCCATATAATTTCTATCTGTGT
 GCAGACAGGTCATCTGTCAACCCTAACCTCTCTGGATGCTCTTTTCTCTGGGACACTG
 TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATCTGGAACCTCATTAATAAATTT
 AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACACAGTAGAAAAAG
 CACATGACTGGATTTTCTGTTTGCCACATCCCTGGACTCAGTTGCTTATTGTGTAATGGA
 TGTGGTCTCTAAAGCCCTCATTTGTTTTGATTGCCTTCTATAGGTGATGTGGACACTGTG
 CATCAATGTGCAGTGCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATCAGGT
 TTTCAAACCAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAAATGCTGTTGT
 GGCCGGGCGCGGTGGCTCACGCCGTGTAATCCAGCACTTTGGGAGCCGAGGCCGGTGATT
 ACAAGGTCAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAAATCCTGTCTTAATAAAAAAT
 AAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCAGCTACTCGGGAGGCTGAGGC
 AGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTGCAGTAAGCCAAGATCACACCCTGCAC
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 18

MRPLLGLLLVFAGCTFALYLLSTRLPRGRRLGSTEAGGRSLWFPSDLAELRELSEVLREYR
KEHQAYVFLFCGAYLYKQGFAPGSSFLNVLAGALFGPWLGLLCCVLTSGVATCCYLLSS
IFGKQLVVSYPDPKVALLRKVEENRNSLFFLLFLRLFPMTPNWFLNLSAPILNIPVQFF
FSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKLLAIAMVALIPGTLIKKFSQKHLQ
LNETSTANHIHSRKDT

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

090306-11101

FIGURE 19

CCGAGGCGGGAGGAGCCCGAGGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTT
CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAACGCCAGCTCAGAA
TAGGAAAATAACTTGGGATTTTATATTGGAAGACATGGATCTTGCTGCCAACGAGATCAGCA
TTTATGACAAACTTTCAGAGACTGTTGATTGGTGAGACAGACCGGCCATCAGTGTGGCATG
TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAAGAAATGAACCTCAGAGACC
CCCCCGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT
TGCTCACTGCCTACTTTGTGATTCAACCTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTCT
GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAA
GAAGTACATGTCAGAAAATAAGGGAGTTCTCTGCATGGGGGTGATGAAGACAGACCTTTC
CAGACTTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCCTGCC
AACTGCACTGGCTGTGCCCAGAAAACACCTGAAGGTGATGTCCTGGAAGACGCCCCAAGGAA
ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCTGTTGGAGGAAGAGATTC
AGCATTTTTTGTGCCAGTACCCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCCAAG
TGGTGGCGCTGCTTTCCTGAGCGGTGGTTCCCATTTCTTATCCATGGAGGAGACCTCTGAA
CAGATCACAAATGTTACGTGAGCTTTTCTGTTTTCACTCACCTGCCATTTCCAAAAGATG
CCTCTTTAAACAAGTGCTCCTTCTTCACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAG
ATGCCTGACCTATTTATCATTGGCAGCGGTGAGGCATGTTGCAGCTCATCCCTCCCTTCCA
GTGCCGAAGACATTGTGAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTG
ACACCACCCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGAT
GGAACCGCTTTCTCAGAAGTTAGGAAAATAGAAGTGTGCACAGGAACAGCTTCAGAGCCGA
AAACCAGGTTGAAAGGGGAAAAATAAAAACAAAAACGATGAAACTGCAAAAA

FIGURE 20

MDLAANEISIIYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPPYPLLIVVY
KVLATLGLILLTAYFVIQPFSPLAPEPVLSGAHTWRSLIHHIRLMSLPIAKKYMSENKGVPL
HGGDEDRFPDFDPWWTNDCEQNESEPIPANCTGCAQKHLKVMLEDAPRKFERLHPLVIKT
GKPLLEEEIQHFLCQYPEATEGFSEGFFAKWWRCFPERWFFPYWRRPLNRSQMLRELPV
FTHLPFPKDALNKCSSLHPEPVVVGSKMHKMPDLFIIGSGEAMLQLIPPFQCRRHCSVAMP
IEPGDIGYVDTTHWKVYVIARGVQPLVICDGTAFSEL

FIGURE 21

CCACGGTGTCCGTTCTTCGCCCCGGCGGCAGCTGTCCCCGAGGCGGGAGGAGCCCCGAGGGGCG
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTTCCAGTTCTCAGCCGTTTCAGTTGTGATC
AAGGGACACGTGGTTTTCCGAACCTGCCAGCTCAGAATAGGAAAATAACTTGGGATTTTATATT
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTTATGACAAACTTTCAGAGACTGTTG
ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAGAGAAGGCAATTGAAAAATTTATC
AGACAGCTGCTGGAAGAATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT
TGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCACTGCCTACTTTGTGATTCAAC
CTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

FIGURE 22

CCCACGCGTCCGCCACGCGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG
 CAGGGTCCCCACTTGCAGCTGCAGCAGCTGCAGAGCGCTGCTCCTGGCTGGTG
 CCCTGCTGGCAGCCTGCTAGACCGTGTCTGAGCGCTGGGGCTGCAGTGGGGACTGCC
 CTCCTCGCCACCCCAATTGTCAGCCCCACCTTCTTTGAAGACTTCAGGCTTTTGTGCCA
 CACCCGAATGGCCCACTTCGACAAACAGGTACAGCCAACTGTCCTCCAGTTTGGAAATG
 GACACGTTATGCTAAGAGCCAGCACCCTTATGTCAGGTTTCTGGAATGCTGCTATGACATGCT
 TATGAGCAGTGGGACAGCGCGCAGTGGGAGCGCGCCAGAGTCTGCTGGGCTTCCAGGAGC
 TGGTGTGGAACCTGCGCAGAGGCGGGCGCGCTGGAGGGCTACGCTACACGGCAGTGCTG
 AAGCAGCAGGCAACGCAGCACTCCATGGCCCTGCTGCAGTGGGGGCGCTGTGGCGCAGCT
 CGGCAGCCATGTGGGGCTGGGCGCTGAGGGACACTCCCATCCCCGCTGGAACCTGCCA
 GCGCCGAGACATATTACGCATGCGTCTGAAGCTGGTGCCCAACCATCACTGCACCTGCAC
 CTGGAAGCCAGCGCTCTCCGAGACAATCTGGGTGAGGTTCCCTTGACACCCACCGAGGAGGC
 CTCACTGCTCTGGCAGTGACCAAAGAGGCCAAAGTGAGCACCCACCAGTTGCTGCAGG
 AGGACAGCTCGCGAGGACGAGCTGGCTGAGCTGGAGACCCGATGGAGGCGACGAACTG
 GATGAGCAGCGTGAGAAGCTGGTGTCTCGCGGAGTGCCAGCTGGTGACGGTAGTGGCCGT
 GGTCCCAGGGCTGCTGGAGGTACACACAGAATGTATACTTCTACGATGGCAGCACTGAGC
 GCGTGGAAACCGAGGAGGCGCTCGGCTATGATTTCGGCGCCCACTGGCCAGCTGCGTGAG
 GCTCCACTCGCGCGCTTCAACCTGCGCCGTTCAGCACTTGAGCTCTTCTTATCGATCAGGC
 CAACTACTTCTCAACTTCCCTGCAAGTGGGACGACCCAGTCTCACTCTCTAGCCAGA
 CTCGAGACCCAGCTGGGCCCATCCCAACCCATACCCAGGTACGGAACCGAGTGTATCTG
 TGGCTCTCGGCCCTACGCCGCCCTCTCAAGGCTACCTAAGCAGCCGCTCCCCAGGAGAT
 GCTGCGTGCTCAGGCTTACCCAGAAATGGGTACAGGCTGAGATATCCAATCTCGAGTACT
 TGATGCAACTCAACACCATTTGCGGGGCGGACCTACAAATGACCTGTCTGACTACCTGTGTT
 CCTGGTCTGTCAGGACTACGTGTCCCCAACCTGGACCTCAGCAACCCAGCGCTGTCCG
 GGACCTCTTGAAGCCTCGGTGTGGTGAACCCCAAGATGCCAGCTCGTGAGGAGGAAGT
 ATGAAAGCTTGGAGACCCAGCAGGACCATTGACAAGTTCCACTATGGCAACCCCACTCTCC
 AATGACGACGCGTGATGCACTACCTCATCCGCTGGAGCTTCACTTCCCTGACGTCGA
 GCTGCAAGTGGCGCTTGTGACTGCTCCGACCGCAGTTCCTCGGTGGCGGAGCTGGC
 AGGCACGCTGGAGAGCCTGCCGATGTGAAGGAGCTCATCCGGAATCTTCTACTTTCCCT
 GACTTCTGGAGAACGAGAACCGTTTGTGACTGGGCTGTCTCCAGTGAACCAAGAGAGGT
 AGGCGATGTGGTGCTACCCCGTGGGCGAGCTCTCCTGAGGACTCATCCAGCAGCACCGCC
 AGGCTCTGGAGTGGGAGTATGTGTCTGCACACCTACACGAGTGGATCGACCTCATCTTTGGC
 TACAAGCAGCGGGGGCGAGCGCGCAGGAGGCGCTCAATGTCTTCTATTACTGCACTATGA
 GGGGGCTGTAGACCTGGACCATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCATTA
 TCAGCAACTTTGGGCGACTCCCTGTCAGCTGCTGAAGGAGCACATCCAATCGGCTCTCA
 GCTGGAGGAGCAGCCCATCGCCTTGACAGCCTGGACACTAATCACTAGCATCTTCCGAGA
 CCTGGACGAACCTCAAGGCATTCTTCGACAGGTTGACTGTGAGTGCCAGTGGGCTGCTGGGCA
 CCCACAGCTGGTTGCCCTATGACCGCAACATAAGCAACTACTTCAGCTTCAGCAAAAGACCCC
 ACCATGGGCGAGCCACAAAGCAGCAGCACTGCTGAGTGCGCCGTGGGTGCCAGGCGTGGTGT
 GAGTGGACAAGCAGTGGCAGTGGCCCGGATGGAAGAGCTGCTATTTCAGCGGTGGCCACTGGG
 ATGGCAGCTGCGGGTGACTGCACTACCCCGTGGCAAGCTTTGAGCCAGCTCAGCTGCCAC
 CTTGATGTAGTAACCTGCTTGCATGGACACCTGTGGCATCTACCTCATCTCAGGCTCCCG
 GGACACACGCTGATGGTGTGGCGGCTCCTGCATCAGGTTGGTCTGTGAGGCTGGGAC
 CAAAGCCTGTGCAGCTCTGTATGGGCACTGGGGCTGCAGTGAGCTGTGTGGCCATCAGCAT
 GAACTTGACATGGCTGTGTCTGGATCTGAGGATGGAATGTGATACACACTGTACCGCG
 CGGACAGTTTGTAGCGGCACTACGGCTCTGGGTGCCACATTCCTTGAGCACTATTTCACCC
 TGGCATTTGGGTCCGAAGCCAGATTGTGGTACAGAGCTCAGCGTGGGAACAGTCTGGGGCC
 CAGGTCACTTCTTGCACCTGTATTCAGTCAATGGGAAGTTGCGGGCTTCACTGCCCCCT
 GGCAGAGCAGCTACAGCCTGACGGTGACAGAGGACTTTGTGTTGTGTTGGGACCGGCCACT
 CGCCCTGCACTCTTCAACTAAACACACTGCTCCCGGCCGCGCTCCTTGTGCCATGAAG
 GTGGCCATCCGAGCGTGGCCGTGACCAAGGAGCGCAGCCAGCTGCTGTGGGCTGGAGGA
 TGCGACGCTATCGTGGTGGTGGCGGGGAGCCCTCTGAGTGGCAGAGCAGGAGTTGCGCG
 GGAAGCTGTGCGGCTCTTTCGCGGCGCATCTCCAGGTGTCCTCGGGAGCAGGAATACAC
 CCTACTGAGGCGCGCTGGAAGCTGGCCAGTCCGGCTGCTCGGGCCCCCGCCGAGGCGCTGA
 GCCCAGGCGCCCGCCGAGAGTGGCGGGGAGAACCCCGGGTGGGACGCCAGGGGGTGA
 GCGGGGCCCCACCTGCCAGCTCAGGAGATTGGCGGGCATGTACCCCTCAGGAGTTGGCG
 GCGGGAAGTCCCGCCCTCGCGCGCTGAGGGGCCGCGCTGAGGCGCAGCACTGGCGCTG

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FIGURE 23

MSQFEMDTYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLEGL
 RYTAVLKKQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLKLVPN
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELAELTP
 MEAAELDEQREKLVLSAECQLVTVVAVVPGILLEVTQNVYFYDGSTERVETEEGIGYDFRRP
 LAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQPPIPHTQV
 RNQVYSWLLRLRPSPQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQLNTIAGRTYNDL
 SQYPVFPWVLQDYVSPFTLDLSNPAVFRDLSKPIGVVNPKHAQLVREKYESFEDPAGTIDKFH
 YGTHYSNAAGVMHYLIRVEFPTSLHVQLQSGRFDCSDRQFHSVAAAWQARLESADVKELIP
 EFFYFPDFLENQNGFDLGCLQLTNEKVGDDVLPWPASSPEDFIQHRQALESEYVSAHLHEW
 IDLIFGYKQRGPAAEEALNVFYCTYEGAVDLDHVTDERERKALEGIISNFGQTPCQLLKEP
 HPTRLSAEEAAHRLARLDTNSPSIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF
 SFSKDPMTGSHKTQRLLSGPWPVPGSGVSGQALAVAPDGKLLFSGGHWGDSLRVTALPRGKLL
 SQLSCHLDVVTCLALDTCGIYLISGSRDTCMVWRLRHQGGLSVGLAPKPVQVLYGHGAAYS
 CVAISTELDMAVSGSEDTVIIHTVRRGQFVAALRPLGATFPGPPIFHLALGSEGQIVVQSSA
 WERPGAQVTYSLHLYSVNGKLRLASLPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA
 PPLEMKVAIRSVAVTKERSHVLVGLLEDGKLIVVVAGQPSEVRSSQFARKLWRSSRRISQVSS
 GETEYNPTEAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
 873-879, 912-918, 954-960

FIGURE 24

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAAATAACATCATGCAACCC
CACGGCCACCTTTGTAACTCCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCAT
CCAAAGGCCTAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCTGGGGCTCTTC
TGGACCCTTAACTGGGTACTGGCCCTGGGCCAATGCGTCTCTGCTGGAGCCTTTGCCTCCTT
CTACTGGGCCTTCCACAAGCCCCAGGACATCCCCTACCTTCCCCTTAACTCTGCCTTCATCC
GCACACTCCGTTACCACACTGGGTCATTGGCATTGGAGCCCTCATCCTGACCCCTTGTCAG
ATAGCCCGGGTCATCTGGAGTATATTGACCACAAGCTCAGAGGAGTGCGAACCCTGTAGC
CCGCTGCATCATGTGCTGTTTCAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCC
TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA
AATGCGTTTCATGCTACTCATGCGAAACATTGTGAGGGTGGTGTCTGGACAAAGTCACAGA
CCTGCTGCTGTTCTTTGGGAAGCTGCTGGTGGTCGGAGGCGTGGGGGTCTGTCTCTCTTTT
TTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAGACTTAAAGAGCCCCACCTCAACTATTAC
TGCGTGGCCATCATGACCTCCATCCTGGGGGCCCTATGTCATCGCCAGCGGCTTCTTCAGCGT
TTTCGGCATGTGTGGACACGCTCTTCTCTGCTTCTCTGGAAGACCTGGAGCGGAACAACG
GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC
GAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGAAGCTCCGGCCCTGATCCAGGACTGC
ACCCACCCCCACCGTCCAGCCATCCAACCTCACTTCGCCCTTACAGGTCTCCATTTTGTGGT
AAAAAAAGGTTTTAGGCCAGGCGCGTGGCTCACGCCGTGAATCCAACACTTTGAGAGGCTG
AGGCGGGCGGATCACTGAGTCAGGAGTTCGAGACCGCCTGGCCAACATGGTGAAACCTCC
GTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCATCCCAGCTAC
TCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGAGA
TCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAAACAAACAAACAA
AAAGATTTTATTAAAGATATTTTGTTAACCT

FIGURE 25

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLGLEF
WTLNWWLALGQCVLAGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQ
IARVILEYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAK
NAFMLLMRNIVRVVLDKVTDLLFFGKLLVVGGVGLSFFFFSGRIPGLGKDFKSPhLNYY
WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNGSLDRPYMKSLLKILGKKN
EAPPDNKKRKK

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FIGURE 26

GAGTCTTGACCGCCGCCGGGCTCTTGGTACCTCAGCGCAGCGCCAGGCGTCCGGCCGCCGT
 GGCTATGTCGTGTCCGATTTCCGCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCC
 TTCTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCGCTTGTTC
 CAGTGTGACCACGTGCAATATACGCTGGTTCAGTTTCTGGGTGGCAAGAACTTGAAACTGC
 ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAAACTGTGGAGCTAATGTAG
 ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGTGACTCCCATAGG
 CCAGTCAATGTCGTCAATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGA
 TGACCTTGAAGTTCGCCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT
 CAGGAAATGACAGTGATGGGTGAGGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA
 GTGGAGCAAACCATGCGGAGGAGGCGCGGAGAGTGGGAGGCCCGGAGAAGAGACATCCT
 CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG
 CTTGGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC
 CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTCTGCAGCG
 CCACGTTTCCCGCCACAACCACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA
 CACGGATCTCCTTTGAGTATGACCTCCGCCTGGTGCTTACCAGCACTGGTCCCTCCATGAC
 AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA
 GCGGCTCCAGGAGTTCCTTGCAGACATGGGTCTTCCCTGAAGCAGGTGAAGCAGAAGTTC
 AGGCCATGGACATCTCCTTGAAGGAGAATTTGCGGGAATGATTGAAGAGTCTGCAAAATAAA
 TTTGGGATGAAGGACATGCGCGTGACAGACTTTCAGCATTCATTTTGGGTTCAAGCACAAAGTT
 TCTGGCCAGCGACGTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT
 CAGGGACAGATCACTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG
 TACCATGGCCTGGAACCTCGCCAAGAAGCAGCTGCGAGCCACCCAGCAGACCATTGCCAGCTGC
 CTTTGACCAACCTCGTCATCTCCAGGGGCTTTCTGTACTGCTCTCTCATGGAGGGCAC
 TCCAGATGTCATGCTGTTCTTAGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCA
 AGTCCTTTGTGTGTTFCAGCAAAGAACC GGCGCTGCAAACCTGCTGCCCTGGTGATGGCTGCC
 CCCTGAGCATGGAGCATGGCAGAGTACCGTGGTGGGCATCCCCCAGAGACCGACAGCTC
 GGACAGGAAGAACTTTTTTGGGAGGGCGTTTGAGAAGGCAGCGGAAAGCACCAGCTCCCGGA
 TGCTGCACAACCATTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT
 CTGGACGCACTTATTTCCCTCCTGTCTTAGGAATTTGATTCTTCCAGAATGACCTTCTTATT
 TATGTAAGTGGCTTTCATTAGATTGTAAGTTATGGACATGATTTGAGATGTAGAAGCCATT
 TTTTATTAAATAAAATGCTTATTTTAGGAAA

FIGURE 27

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAF
LEHKEQFHYFILINCGANVDLLDILQPDEDITIFFVCDSHRPVNVVNVYNDTQIKLLIKQDDD
LEVPAIEDIFRDEEEDEEHSGNDS DGSEPSEKTRLEEEIVEQTMRRRQRREWEARRRDILF
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGVLRH
VSRHNHRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSL CNTSYTAARFKLWSVHGQKR
LQEF LADMGLPLKQVKQKFQAMD ISLKENLREMIEESANKFGMKDMRVQTF SIHFGFKHKFL
ASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCL
CTNLVISQGPFLYCSLMEGTPDVMLFSRPASLSLSKHLKSFVCSTKNRRCKLLPLVMAAP
LSMEHGTVTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNHFDLSVIELKAEDRSKFL
DALISLLS

FIGURE 28

GTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCGTGGCTATGNTCGTGTCCGATTTCCGCA
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTTCTCTTCGTGGCCTCGGANGTGGAT
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAGTGTGACCANGTGCAATATANGCT
GGTTCAGTTTCTGGGTGGCAAGAACTTGAAACTGCATTTCTTGAGCATAAAGAACAGTTTC
ATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT
GAAGACACTATATTCTTTGTGTGTGACACCCATAGGCCAGTCAATGTTGTCAATGTATACAA
CGATACCC

FIGURE 29

CAGGAACCTCTCTTTGGGCTGGATTGGGACCCCTTTCCAGTACCATTTTTCTAGTGAAC
 CACGAAGGGAGCATACCAGAAAACACCTCAACCCAAAGGAAATAGACTACAGCCCCAATTG
 GCTGACTTTGGCTATAGAAAAAAGAAAGAACGAAAAGACAGTATTTTTTGGAAAGCTAA
 GTCTTCCCTTTATCGAGTCAAGAAACCCCCCTTCTTGAGCTATTTACAGCTTTTAAACAAAT
 GAGTAAAGTAGCTCCCGTCAAC**ATGGT**GACAGCGCCCTGGTCCGCTGGGCAGGCCTC
 CTGCTCTTTCTCTGATGTGTGAGATCCGTATGTGTGGAGCTACCTTTGACAGAGCTGTGGC
 CAGCGGCTGCCAACGGTGTGTGACTCTGAGGACCCCTGGATCTGCCATGATCTCTCAG
 CCTCTTCTCGCGCGCCCGCCAGCCCTGCTGAGATCAGACCCATACATTAATATCACCATC
 CTGAAGGGTGACAAAGGGGACCCAGGCCCAATGGGCCTGCCAGGGTACATGGGCAGGGAGG
 TCCCCAAGGGGAGCCTGGCCCTCAGGCGAGCAAGGGTGACAAAGGGGAGATGGGCAGCCCCG
 GCGCCCCGTGCCAGAACGCTTCTTCCGCTTCTCAGTGGGCGCAGAACGGCCCTGCACAGC
 GGCAGGAGACTTCCAGACGCTGCTCTTCCAAAGGGTCTTTGTGAACCTTGATGGTGCTTTGA
 CATGGGCACCGCCAGTTTGTCTCTCCCTTGCCTGGCATCTACTTCTCAGCCTCAATGTGC
 ACAGCTGGAATTACAGGAGACGTACGTGCACATTATGCATAACCAGAAAGAGGCTGTATC
 CTGTACGCGCAGCCCAGCGAGCGCAGCATCATGCAGAGCCAGAGTGTGATGCTGGACCTGGC
 CTACGGGACCGCGTCTGGGTGCGGCTCTTCAAGCGCCAGCGCAGAACGCCATCTACAGCA
 ACGACTTCGACACCTACATCACCTTACGCGGCCACTCATCAAGCGCCAGGACGAC**AGGGG**
 TTTCTGGGCCACCCCTCCCGGCTGGAGAGCTCAGGTGCTGGTCCCGTCCCTCTCAGGGCTCAG
 CTTTGACTGCTGTGAAGCAGGAGGCCAGGGAGTCTCCCGGGACCTGGCATCTGGGGAGA
 CCGTGCTTTCTATCTTGGCTGCCATCATCCCTCCAGCCTATTTCTGCTCTCTCTCTCTCT
 TGGACCTATTTTAAAGAGCTTGCTAACCTAAATATCTAGAACCTTTCCAGCCTCGTAGGCC
 AGCACTTCTCAAACCTTGGAAATGCATGCGAATCACCCGGGGTTCGTGTTAAATCGAATTTCT
 GACTCAGCAGTCTGAGTGGGTCCAGGATTCTGTGTTCTCATATCTCTGGGTGATGCTG
 ATGGGGTCAGTCTATGAACCACACTGGAGCAACAGGTTCTAGGACTTTCTCAATATCTAG
 TACTTTCTGAACATTTCTGGAATCTCCACATTTAGAAATCTCCCAACATTTTTTTTTCT
 TGAGACAGAGTCTTGTCTGTTGCCAGGCTAGAGTGCAGTGGTGCATCTCAGTTCTACTGC
 AACCTCTGCCCTCCCGGTTCAAGCGATTCTTCTGCTCAGCCTCCCTAGTGCGCTGGGATTAC
 AGGCGCTGCTACCATGCTTGGCTAATTTTTGTATTTTGTAGAGAT3GGGTTTACACATA
 TTGGCCAGGCTGGCTTGAACCTCTGACTTCAAGGTGACCCACCGGCTCGGCCTCTCAAAAT
 GCTGGGATTACAGGTGTGAGGCCACCGTGCTTGGCCAATTCCAACTTTCTAAATTTCTCTCAT
 CCTCCAGGGCTCCCGTGCTATGTTCTCTTTACCCCTTCCCTCTTCTCTTGTCTCAGGCC
 TGCACCACTGCAGCCACCGTTCAATTTATTCATTATTAACACTGAGCACTCAGTCTGTGCT
 GGGTCCCGGGAAGGGTGAGGGGGTGCAGACACAGGCCCTGCCCTGCCCTCAGTGACTGGCCA
 GTCCAGCCACAGCGGGGAGAGATGTGTACATAGGTTTTAAAGCAGACCAGAGCTCATGGGG
 GCCTGTGTTCTGGGTGTTTCAGGTGCTGCTGGTCTCCATTACCCACTGCTCCCCAAGGCTGG
 TGGGACGGGGTCCCGGTGTCAGGGGCAGGTATCTCTTCCCGTTCTCTATCCACTTCCCCGAG
 TGCTCATCGTTACAGCAAAACCCAGGGGGCTTGGCCAGGTCAAGGGTTCTGTGAGGAGAGG
 ACCCAGGAGTGTGGGGGCAATTTGGGGGGTGAAGTGGCCCCGAAGAATGGAACCCACACCA
 TAGCTCTCCCCACAGCTGATACGGCATCTTGCAGAGAAGACTGCCCTCTCAGTGGGATCC
 CTCTCTGCTCTCTCCAGGGCTCTGCCAGGGCCTTGCTCAGTCCCTTCCACCAAGTCTATCT
 GAACCTCCGTTTCCCCAGGGCTCCAGCTGCCCTCAGACACTGATGATCTGTCTCCCAAGTGCT
 CTCTGCCCTCATGCCCTCTCACCAGGCCAGTGCCCCGACTCTCCAGGCTTTATCAGGTTG
 CTAAGGCCGGGTGGGCTCCTGCTCTCAGAGCCCTCTCCGCTGGTGGTGGCTCTTTAC
 AAACACCTCGAGGAGAAGGGCCACGGAAGCCCCAGGCTTTAGAGCCCTCAGCAGGTCTGGGG
 AGCTAGAGCAAAAGGAGGACCTCAGGCCCTTCCGTTTTCTTCTCCAGGGTGGGTGGCTGCTC
 GTTCCCTAGCCCTTCCAACCCAGGTGGCTGCCCTTCTCCCGAGAGGAGGGGCTCCCG
 CCATTTGTGCTCATGACAGTCTGGGGCTGAGGTGCCCGGGGGGTGATCTCTGGTCTCAC
 AGCCGAGGGAGCCGTGGCTCCATGCCAGATGACGGAACAGGGTCTGACCAAGTGCCAGGA
 AGACCTGTGCTATAAACCACTTGCCTGATCCTGCCCTGCTGACCCGCGCACGCCCTGCC
 GTCAGCATGATTAAGAATGCTGTCTCTTGGAAAAAAAAAAAAAAAA

FIGURE 30

MVTAALGPFVWAALLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSGRPH
ALPEIRPYINITILKGDKGDPGPMGLPGYMGREGPQGEPGPGQSGDKGEMGSPGAPCQKRF
FAFSVGRKTALHSGEDFQTLLFERVFNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET
YVHIMHNQKEAVILYAQPSESRIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYIT
FSGHLIKAEDD

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation site.

amino acids 72-75

Clq domain proteins.

amino acids 144-178, 78-111 and 84-117

ACTCGAACGCAGTTGCTTTCGGGACCCAGGAACCCCTCGGGCCGACCCGCCAGGAAAGACTG
AGGCCGCGGGCTGCCCGCCGGCTCCCTGCGCCGCGCCGCTCCCGGGACAGAAAGTGTG
TCTCAGGGTCCCTCTGCTGCTGCTCCGCTGCTCTGCTACGTCCCTGGGGCTCGGGGTGCAG
GCTGCCCATCTCCGGTGCACAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCCGCCAGGGG
ACCAACGGTGCCCGAGACAGTGCACCCGACACGGTGGGGCTGTACGCTCTTTGGAACCGGCAT
CACCATTGCTGCACGAGCAGCTTTGCCCGCTGCCGGGCTCGAGCTCTTGACCTTGCTAC
AGAACCAGATCGCCAGCTGCCGAGCGGGGTCTTCCAGGCACCTGCACAACCTCAGCAACCTG
GACCTGACGGCCAAACAGCTGCATGAATACCAATTGAGACCTTCCGTGGCTCGCGGCC
CGAGCGCCTCTACCTGGGCAAGAACCGCATCCGCCACATTCAGCCTGGTGCCCTGCAGACGC
TCGACCGCCTCTTGAGAGCTCAAGCTCAGGCAGACACAGCTCGGGGACCTGCCCGCGCTGCGC
TGCCCGCGCTGCTGCTGCTGACCTCAGGCCACACAGCCTCTTGGCCTGGAGCCCGGCAT
CCTGAGACATGCCAACGCTGGAGGCGCTGCGGCTGGCTGGTCTGGGGTGCAGCAGCTGGACG
AGGGGCTCTTACGCCGTTTGCACAACCTGGAGCTGGATGTGTCGCACAACCACTGGAG
CGAGTGCCACCTGTGATCCGAGGCTTCGGGGCTACGCGCTGCGCTGGCCGGCAACAC
CCGACTTGCCCACTGCGGCGCGAGACACTTGGCCGCGCTGGCTGCCCTCGAGGAGCTGTGAT
TGACAACCTTAAGCTCGAGGCCCTGCTGCGACCTCTCGGCGCTTTCGCCCGCTGCGG
CTGCTGCGAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCCCTGAGCTGGTTCGGCCCTG
GGTGCGCGAGAGCCAGCTCACACTGGCCACGCTTGAGGAGAGCGCTGCCATCTCCCGCCCA
AGAAGCTGGCCGGCTGCTCTTGAGAGCTGACTACGCGACTTTGGCTGCCAGGCCACCC
ACCAACAGCCAGCTGCCCCACCAACGAGGCCGCTGGTGCGGGAGCCACAGCCTTGCTCTTAG
CTTGCTCTCACTGGTCTTAGCCCCACGCGCCGACCTGAGGCCCTAGGCCCGCCCTCA
CTGCCCCACCGACTGTAGGGCCTGTCCCCAGCCCGAGACTGCCACCGTCCACTGGCT
AATGGGGGACCACTGCCACTGGGGACGCGCACCACTGGGCTGCTTTGTGCCCAAGAGCTT
CAGCGGCTGTACTGTGAGACGCAGATGGGCGAGGGACAGGCCACGCCCTACACCATCA
CGCCGAGGGCCACACGCTTCCCTGACCTTGGGCATCGAGCCGCTGAGCCCCACCTCCCTGCGC
TGGGGCTGCAGCGCTACCTCCAGGGGAGCTCCGTGACAGCTCAGGAGCCTCCGCTCTCACTA
TCGCAACCTATCGGGCCCTGATAAGCGGCTGGTGACGCTGCAGCTGCTGCTGCTGCTGCT
AGTACAGCGCTCACCAAGCTCGGCCCCACAGCCCACTTACTCGCTGTGTATGCTCTTGGGG
CCCGGCGGGTGCGGAGGGCGAGAGGCTGCGGGGAGGCCCATACACCCCAAGCCGCTCA
CTCCAAACCAACGCCCCAGTACCCAGGCCCGCGAGGGGCAACCTGCCGCTCTCTATTGCGCCC
CCCTGGCCGCGGTGCTCTTGCCCGCGCTTGCTGCGTGGGGGACGCTACTGTGTGCGGCG
GGCGGGGCTATGCAGCAGCGGCTCAGGACAAGGGCAGGTGGGGCGAGGGCTGGGCCCT
GGAATCGGAGGAGTGAAGGTCCTTGTAGGCCAGCCCGCAAGGCCAACAGAGGGCGGTGGAG
AGGCCTGGAGGCGCGGTCTGAGTGTGAGTGGCACTCATGGGCTTCCCAGGGCTGGCCT
CAGTACCCCTCCACGCAAAGCCCTACATCTAAAGCCAGAGAGAGCAGGGCAGCTGGGCGG
GGCTCTTCAGGCAGTGAGATGGCCAGCCCTCTGCTGCCCACACAGCTAAGTTCTTCAGTCC
CAACTTCGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCGTGTTCCTCTGGA
CTCTGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCAGAAC
CGAGTGCTTATGAGGACAGTGTCCGCCCTGCCCTCCGCAAGTGCAGTCCCTGGGACGGCG
GGCCCTGCCATGTGCTGGTAACGATGCTGGGTCTGCTGGGCTTCCACTCCAGCGGCA
CGCTGGGGGCGGAGTGAAGGAAGCTCCCGGAAGACGAGGAGGAGCGGGTGGCGGCTGTG
TGACTCTAGTCTTTGGCCCGAGAGCGAAGGAACAAAGAACTGGAAGGAAGATGCTTTA
GGAACATGTTTTGCTTTTTTAAAAATATATATATTTATAAGAGATCCTTTCCATTATTCTG
GGAAGATGTTTTTCAACTCAGAGACAAGCACTTTGGTTTTTGTAGACAACCATGATATG
AAGGCTTTTGTGAAGAAAAATAAAGATGAAGTGTGAAA

FIGURE 32

MCSRVP LLLPL LLL L L L L L A L G P G V Q G C P S G C Q C S Q P Q T V F C T A R Q G T T V P R D V P P D T V G L Y V F E N
G I T M L D A G S F A G L P G L Q L L D L S Q N Q I A S L P S G V F Q P L A N L S N L D L T A N R L H E I T N E T F R G L R
R L E R L Y L G K N R I R H I Q P G A F D T L D R L L E L K L Q D N E L R A L P P L R L P R L L L L D L S H N S L L A L E P
G I L D T A N V E A L R L A G L G L Q Q L D E G L F S R L R N L H D L D V S D N Q L E R V P P V I R G L R G L T R L R L A G
N T R I A Q L R P E D L A G L A A L Q E L D V S N L S L Q A L P G D L S G L F P R L R L L A A A R N P F N C V C P L S W F G
P W V R E S H V T L A S P E E T R C H F P P K N A G R L L L E L D Y A D F G C P A T T T T A T V P T T R P V V R E P T A L S
S S L A P T W L S P T A P A T E A P S F P P S T A P P T V G P V P Q P Q D C P P S T C L N G G T C H L G T R H H L A C L C P E
G F T G L Y C E S Q M G Q G T R P S P T P V T P R P P R S L T L G I E P V S P T S L R V G L Q R Y L Q G S S V Q L R S L R L
T Y R N L S G P D K R L V T L R L P A S L A E Y T V T Q L R P N A T Y S V C V M P L G P G R V P E G E E A C G E A H T P P A
V H S N H A P V T Q A R E G N L P L L I A P A L A A V L L A A L A A V G A A Y C V R R G R A M A A A A Q D K G Q V G P G A G
P L E L E G V K V P L E P G P K A T E G G E A L P S G S E C E V P L M G F F G P G L Q S P L H A K P Y I

FIGURE 33

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGAAGCCGTGGGGGTTTTGAGCTCAT
 CTTTCATCATATGAGGAAATAAGTGGTAAAACTCCTTGGAAATACAATGAGACTCATCAG
 AATCATTTACATATTTTGTAGTATTGTTATGACAGCAGAGGTGATGCTCCAGAGCTCCGAG
 AAGAAAGGGAATGATGACCAACTGCTCCAACATGCTCTAAGAAAGGTTCCCGCAGACTTG
 ACCCGACGCCAACGACGACTGGATTTATCCTATAACCTCCTTTTCAACTCCAGAGTTTCAGA
 TTTTCATTCTGCTCCAACTGAGAGTTTGTTGTTCTATGCCATAACGAATTTCAACAGCTGG
 ATCTCAAAACCTTTGAATTCACAAAGGAGTTAAGATATTTAGATTGTCTTAATACAGACTG
 AAGAGTGTAACCTTGTATTACTGCGAGGCTCTCAGGTATTTAGATCTCTCTTTTAATGACTT
 TGACACCATGCTTATCTGTGAGGAAGCTGGCAACATGTCACACCTGGAAATCCTAGGTTTGA
 GTGGGGCAAAAAATCAAAAAATCAGATTTCCAGAAAAATGCTCATCTGCATCTAAATACTGTC
 TTCTTAGGATTTCAGAACTCTCTCCTATTATGAAGAAGGTAGCCTGCCATCTTAAACACAAC
 AAAACTGCACATTGTTTTACCAATGGACACAATTTCTGGGTTCTTTTGGGTGATGGAATCA
 AGACTTCAAAAAATATTAGAAATGACAAATATAGATGGCAAAAGCAAAATTTGTAAGTTATGAA
 ATGCAACGAAATCTTAGTTTAGAAAAATGCTAAGACATCGGTTCTATTGCTTAATAAAGTTGA
 TTTACTCTGGGACGACCTTTTCTTTATCTTACAATTTGTTGGCATACATCAGTGAACACT
 TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAATTCATTGACTAC
 TCAAAATCTGTAATGAGAATATAAAATGGAGCATGTACATTTACAGAGTGTTTTACATTCA
 ACAGGATAAAAATCTATTGCTTTTGACCAAAATGGACATAGAAAACCTGACAATCTCAAAATG
 CACAAATGCCACACATGCTTTTTCCGAAATATCCTACGAAATTCCTAATTTTAAATTTTGGC
 AATAATATCTTAAACAGACGAGTTGTTTAAAGAATCTTCAACTGGCTCTGCTGAAAACCTCT
 CATTTTGAATGGCAATAAATCGAGACACTTTCTTTAGTAAGTTGCTTCTGCTAACACACAC
 CCTTGGAAACCTTGATCTGAGTCAAAATCTATTACAACATAAAATGATGAAAATTTGCTCA
 TGCCCAAGAACTGTGGTCAATATGAATCTGTACATAAATAAATGCTGTGCTGCTCTCAG
 GTGCTTGCCCAAAAGTATTCAAACTCTGACCTAAATAAATACCAAAATCAAACCTGTACCTA
 AAGAGACTATTCATCTGATGGCCTTACGAGAATAAATATTGCAATTTAATTTTCTAAGTAT
 CTCCCTGGATCGAGTCATTTGAGTAGACTTTCAGTTCTGAACATTGAAATGAACTTCTATTCT
 CAGCCCAATCTCTGGATTTTGTTGAGAGCTGCCAGGAAGTTAAAACTCTAAATGCCGGAAGAA
 ATCCATTCGGGTGTACCTGTGAATTAATAAATTTTCATTGAGCTTGAACATATGTCAGAGGT
 ATGATGGTGGATGGTCAGATTATACACCTGTGAATACCTTTAAACCTAAGGGGAACATG
 GTTAAAGAGCTTTCATCTCCACGAATATCTTGAACACAGCTCTGTGATTGTCAACATTG
 TGGTTATTATGCTAGTTCTGGGGTTGGCTGTGGCCTTCTGCTGTCTCCACTTTGATCTGCC
 TGGTATCTCAGGATGCTAGGTCAATGCACACAACATGGCACAGGTTAGGAAAACAACCCA
 AGAAACACTCAAGAGAAATGTCCGATTCACGCATTTATTTATACAGTGAACATGATTTCT
 TGTGGGTGAAGAAATGAATTTGATCCCAATCTAGAGAAGGAAGATGGTTCTATCTGATTTGC
 CTTTATGAAAGCTACTTTGACCTGGCAAAAGCATTAGTGAAATATTGTAAGCTTCAATTGA
 GAAAAGCTATAAGTCCATCTTTGTTTTGTCTCCCACTTTGTCCAGAATGAGTGGTGCCATT
 ATGAATTTCTACTTTTGGCCACCACAATCTCTTCCATGAAAATTTCTGATCATATAAATCTTATC
 TTACTGGAACCCATTTCCATTTCTATTGCATTTCCACAGGATATCAATACTGAAAGCTCTCCT
 GGAATAAAAGCATATTTGGAATGGCCCAAGGATAGGCGTAAATGTGGCTTTTCTGGGCZAA
 ACCCTTCGAGCTGCTATTAATGTAAATGTATTAGCCACCAGAGAAATGTATGAATCGCAGACA
 TTCACAGATTAATGAAGAGCTCTCGAGGTTCTACAATCTCTGATGAGAACAGATTTGCTCT
 TAAAAATCCCAAGTCCTTTGGGAAGTTGGGGACCACTACACTGTTGGGATGTACATTTGATA
 CAACCTTTATGATGGCAATTTGCAATATTTTAAATAAAAAATGGTTATTCCTCTCATAT
 TCAGTTTCTAGAAAGGATTTCTAAGAATGTATCCTATAGAAAACCTTCAACAAGTTTATAAGG
 GCTTATGGAATAAAGGTGTTTCATCCAGGATTGTTTAAATCATGAACATGTGGCCAGGTGC
 AGTGGCTCACTCTTGTAAATCCAGCACTATGGGAGGCCAAGGTGGGTGAGCCACGAGGTCAA
 GAGATGGAGACCATCTTGGCCAACTGTTGAAACCTGTCTCTACTAAAAATACAAAAATTA
 GCTGGGCGTGATGTTGCACGCTGTAGTCCAGCTACTTGGGAGGCTGAGGCAGGGAATTCG
 CTTGAACCCGGGAGGTGGCAGTTGCACTGAGCTGAGCTGAGCCACTGCATCCAGCTGGT
 GACAGCGCAGACTTCCATCTCAAAAAAAGAAAAAAGAAAAAATGAAAAACATCC
 TCATGGCCACAAAAATAGGCTTAATTCATAAATATAGTACATATGATTAATATAATATTA
 CATGCCATAAAAAGATAAGGTAGCTGTATTTTCTGGTATGAAAAACATATTAATAT
 GTTATAAATCTTAGGTTGGTGCAAAACCTAATTTGGTTTGTGCAATGAAATGGCATGTAA
 ATAAAGGTGTAAAGAAATCTATACAGATGTAGTAACAGTGGTTGGGCTCTGGGAGGTGGA
 TTACAGGAGCATTTGATTTCTATGTTGTATTTCTATAATGTTTGAATGTTTAGAATGA
 ATCTGTATTCTTTTATAAGTAGAAAAAATTAAGATAGTTTTACAGCTT

FIGURE 34

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQ
LQSSDFHSVSKLRVLILCHNRIQQDLKTFFFNKELRYLDLSNNRLKSVTWYLLAGLRVLDL
SFNDFDTMPICEEAGNMSHLEILGLSGAKIQKSDFKIAHLHLNTVFLGFRTLPHYEEGSLP
ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL
LNKVDLLWDDLFILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
VFYIQQDKIYLLLTKMDIENLTISNAQMPHMLFPNYPTKFQYLNFANNILTDELFKRTIQLP
HLKTLILNGNKLETLSLVSCFANNTPLEHLDSLQNLLQHKNDENCSPETVVMNLSYNKLS
DSVFRCLPKSIQILDNNNQIQTVPKETIHLMALRELNIAFNFLTDLPGCSHFSRLSVLNIE
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSEVMVGVGSDSYTCEYPLN
LRGTRLKDVHLHELSCNTALLIVTIVVIMLVGLAVAFCLHFDLPWYLRMLGQCTQTWHRV
RKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSI SENI
VSFIEKSYKSIFVLSPNFVQNEWCHYEFYFAHNNLFHENS DHIILILLEPIPFYCIPTRYHK
LKALLEKKAYLEWPKDRRCGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLM
RTDCL

FIGURE 35

GGGGGCTTCTTCTGGGCTTGGCTGCTTGGAACTACTGCTTCCAAGGACGGCCTTGGAGGGGTGCGCGGGAAGG
GAGGAGAAGGAAGGCGGGGCGGGCGCCCTCGCCGCGCCGCGCGCTTGTGCGCGCTTGTGCGCGCGCGG
CCAGCCACGACGACCCCGCGGCGCGCTCACGCGAGCAGCGCGCGCTTCCGCGGCCAACGAGCGCGCT
CTGCTGTGCTTCCGCTTCCGCGCGCGACGTTTGTGGCGCGCAGCGCGCGCGCGCGCGCGCTGACCTGA
CCCTGCCCTTGGCGCGGGCGGGAGCAGG¹ATGTCCGCGCGGGAGCGCTACCCAGCGGTGGCCCTGGTGTCT
CTGGCAGTGCAGCTGGCGCGGCTCGAGCGCGGGAGCGCGACCTTCAGGACCGCTGATTATACGGGACGAGAT
TGTGAGCGAGGCGCTTACTACGCGCCCGAGCGCGAGCTTCAGACCTTCTCTCCGCGCTGCTGTGCGGGG
CCGGGAGGAGATGGGAGCGCGCGCCGACGAGGCGCGAGCGCCAGGAGGCGCCAAACGCGAAGAGCTCCC
AAGAGGAGAAGTGGCTGCGGAGCGCTTCCACAGGTAAACACAGCAACAAAAGTTATGAGAACCAAGT
CTCTGAGAAGGCTGCCACGATGATCAGAGTGTCCGTGTGGCCCGTGAAGATTGTACAGAGAGATTGCCCACT
TTGTGCTTGGAACTTAAAAATCAGACGTTCCAGTCTCATGCTCCACGGTGAAGCGCTATGGCTTGGGGGCA
CATCGAGGAGATCAACATCCAGCGGGCATTAATAAAAAATGATTTTATGACGGCGTGGTGTCCGCGGAAG
AAATGACCTCCAGAGTGGAATGAAGTGGATGCTCGCGCGCTACGACGATCTAGTGTCTATCATCAAGGA
GGAATCCCTCTGTGCTGAGTGATGGTGATACCTTAAGTGCTGAGCAAGTACAGCCACAGTGGGTCT
ACTGTTAAGATGGATGTGAGACATGATATTTGAGGGAACATGAGAGAGAGATCCCTGTCTCATAGAGCT
ACCCGTCCTCCATGTGTGGCCCGCTACATCCGATAAACCTCAGTCTGTGGTTTGATTAATGGAGAGCATGCGATG
GAATGAGATGTCTGGGCTGCCACTGCCAGATCTATAATATTATCCCGCGCGAAGCGAGATGACCCACCT
GATGACCTGGATTTAAGACCCACAATTTAAGGAAATGCGCCAGTGTGAGAAATGTGAATGAATGTGTC
CAATATCAACAAGTTTACAACTTTGAAAGAACCCACCGAGCGCTGAAGCTGTATCGTGTGGAGATCTCAGATC
ACGCTGGGAGCATGAAGTCGTGTGAGCGCGAGTTCCAGTACATCGCGGGGACCGCGCATAGGTTGTGTCGGC
CGGAGCTGCTGCTGTGCTGTGTCAGTTCTGCTGTTCAGGATGATTTGGCCCGGGAATGCGCGCATCTGCCACT
GTGGGAGAGAGCGGAGTTCACTGCTCCCTCGTCAACCCGATGGCTAGAGAGGCGTACGAAGGGGCT
CGAGCTGGGAGGCTGTGCTTCCGTGGAGCTGCGAGCCAGTGAAGATGCAATCAACAACACTTTTCTGATTTA
ACAACGCTGTCTGGGAGGACAGGATCGACAGATCTCCGAGAAATGCCATCATATGCAATTTGCAATCCC
TGAGTGGTTTCTGTGCGAAATTCGACGGTGGCTGCGGACAGCAGGACGATATAGCTCGGTGATGCAAAAAATC
TTTTTGTGCGGGCGCAATTCGAGGCGCGCGAGCTGTGGTGGGAGTATCCCTACAGCTGTGTGCGGTCCCC
TGGAAAGCGCGAGGAACACACCCCCCGGATGACCCAGTGTCCGCTGGTGGCTTACTCTTATGCTCCAC
ACACGCGCTCATGACAGACCCCGGAGGAGGCTGTGCCACGAGGAGCTTCAGAGGAGGAGGGCGCATGTCA
ATGGGGCTCTGGGACACAGCTCGCTGGAAGTGTGAAGCATTTAGCTACCTTATCAACAACGTCATCGAAGT
TCCATCTAGTGGCTGTGATAAATACCACTGAGAGCAGCTGCGCGAGGTGGAGAGATCCCGGGAATC
TCTGATGCTTTATGAGGAGGAGTTCAFTGCTGGCATTAAGGCTTTGTGAGAGATTTGATGTGAAAGAAATCC
CAACGCGCTATCTTCGTGAGAAGCATTAACATGACATCGCAAGCCACAGTACGAGTATCTGCGCGCT
CTGAACCGTGGAGATGTGTGTGCAGCAAGGCGGAGGTTTCACTCATCCACCAAGATCTTATGGTTGTG
CTATGACATGGGGGCGACAGGTGTGATCTTCAACATTCAGAAACCATGCGCAGATCGAGATATCGG
AGAATTTGGGAGACGCGCTCAGCGCTGCCACGACGCGGCTGAAGCTCGCGGGCGGAGAGAGACAGCGCT
GGTGA²CCCTCTGGCGCCTTGAAGCTCTGGGCGAGTCGAAATTAACAACCTGTGATAGTCTCATATG
TGACATGCTCACTGTGTTTCTCTGTATTCAGAAGTGCTGCTGGAAGAGAGGTCGATTTGTAGGACGAGTCC
CAAAAGGAAGGCTGGAGCTGAGGCTGTTTCTTTTCTTGTTCCTTATTCAAATATGCTTGGACAGAGCG
GACGAGAAAGAGTGTAGGAGATGAGAAGACTCAGCAGCGCAACCTCGGAATCAGAGAGAGAGGAGAGAGGG
GAGCTGTCCGCTCAGAGCTCTGCTGTCATGAGAAAGGATTGTGTTGCTCCCTCTGTTTGTGGCAGCAAG
GTTCAGATGTCATTTGCAATTTGCACAGTGAATTAATTCAGCAATTCCTGGCCCTGGGACGTGCAAGCTGTGCAAAATAT
TTTGAAGCTCTCCAGGCGCTCTAAGAGATCAACCCCTCTGGCCCTGGGACGTGTCAGCTTGTGGGACAGCA
ATTCTGTGTTCTTTGACATAGCTCATTTGCCAAGTGACATCAGTAGCGCTCTTGAATCTGTTTAGTCTCTCT
TTTTCACAAAGGAGTGTTTCCAGAAAGAGAGAGAGGAGTGAATCATCAGGATCTTGTGGGACAGCA
TGGAGCTTCTTGACAAATTTTGGGTCGTAAGAACACCCCGAGATCCCTGCTGATCAGCTAGCTCCGCTGGAGTT
CCCCGCTAGGAGAGCGAGGATGCGACGCTCTCTGAAGGCGAGAAATTTAGCTCGGATCTCCTCTTTTAT
CTGCTAGGACTGGAAGAGCGGAAGTGGGTGGCTGAAGCCCTCTCTGCTGTGAGGATGGCCCTGTGTG
GAATTTGAGTGTCTATGGTTGCGCTCATATCAGCTCGGGAGTTTATTTGATGATGAGAATGGCATCTCCA
GATTAGGCTAATATGATGAARAACCTCTAGGATATCTGTGGAGCATGATTTGGGAGAAATTTGAAATTA
CTTCAAGCAAAAGATGATGTTCTCACTTTTGTGTAATGTCTGCTCTGACTGACCTGGGAAATGAAAAA
AATTAAGCAAAATGTGATGACCTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA

FIGURE 36

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPPYARPEPELETFSPPLP
AGPGEEWERRPQEPRPPKRATKPKAPKREKSAPEPPPGKHSNKKVMRTKSSEKAANDDHS
VRVAREDVRESCPPLGLETLKITDFQLHASTVKRYGLGAHRGRLNIQAGINENDFYDGAWCA
GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSHTWVTVKNKSGDMIF
EGNSEKEIPVLNELPVPVMVARYIRINPQSWFDNGSICMRMEILGCPLPDPNNYYHRRNEMTT
TDDLDFKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPEGEHEVGEPEF
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLP SLNPDGYEKAYEGG
SELGGWSLGRWTHDGI DINNFDPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFLSENATVAA
ETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDLVRS PWKTQEHTPTPDDHVFRWLAYSAST
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFS YLHTNCFELSIYVGCDKYPHES
QLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKGIPNAIISVEGINHDIRTANDGDYWRLL
NPGEYVVTAKAEGFTASTKNCMVGYDMGATRCDFTL SKTNMARIREIMEKFGKQPVSLPARR
LKLGRKRQRG

FIGURE 37

CTAAGAGGACCAAGATGAGGCCCGGCTCTCATTTCCTAGCCCTTCTGTTCCTTGGCCAAGCTGCAGGGG
 ATTTGGGGGATGTGGGACCTCCAATTCCCAGCCCCGGCTTCAGCTCTTCCCAGGTGTTGACTCCAGCTCCAGC
 TTCAGCTCCAGCTCCAGGTGGGGCTCCAGCTCCAGCCGAGCTTAGGCGAGCGGAGGTTCTGTGTCACGTTGTT
 TTCCAATTTACCGGGTCCGCGGATGACCGTGGGACCTGCCAGTGCTCTGTTCCTGCCAGACACCACTGTTT
 CCGTGGACAGAGTGGAAACGCTTGAATTACAGCTCATGTTCTTCTCAGAAGTTTGAGAAAGACTTTCTAAA
 GTGAGGGAATATGTCCAATTAATTAGTGTGTATGAAAGAAACTGTTAAACCTAACTGTCCGAATTGACATCAT
 GGAGAAGGATACCAATTTCTTACACTGAACTGGACTTCGAGCTGATCAAGGTAGAAGTGAAGGAGATGGAAAAAC
 TGGTCAACAGCTGAAGGAGAGTTTGGTGGAGCTCAGAAATTTGTGACCACTGGAGCTGGAGATAAGAAAT
 ATGACTCTCTTGGTAGAGAGCTTGAGACACTAGACAAAACAAATGTCTTGGCATTTCGCCGAGAAATCGTGGC
 TCTGAAGACCAAGCTGAAAGAGCTGTGAGGCTCTAAAGATCAAAACACCCCTGTCTGCCACCCTCTCCCACTC
 CAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAAACCGTCTGTGGTTGAGCTCAACTGGAGAGGGTTT
 TCTTATCTATATGCTGCTTGGGGTAGGGATTACTCTCCCGAGCATCCAAACAAAGGACTGTATTGGGTGGCGCC
 ATTGAATACAGATGGGAGACTGTGGAGTATTATAGACTGTACAACACACTGGATGATTGCTATTGTATATAA
 ATGCTCGAGAGTTGCCGGATCACCTATGGCCAGGTAGTGGTACAGCAGTTTACAACAACACATGTACGTCAAC
 ATGTACAACACCGGGAATATTGCCAGAGTTAACCTGACCACCAACACGATTGCTGTGACTCAAACTCTCCCTAA
 TGCTGCCATAATAACCGCTTTTCATATGCTAATGTTGCTTGGCAAGATATTGACTTTGCTGTGGATGAGAATG
 GATTGTGGGTTATTATTCAACTGAAGCCAGCACTGGTAACATGGTGATTAGTAAACTCAATGACACCACACTT
 CAGGTGCTAAACACTTGGTATACCAAGCAGTATAAACCATCTGCTTCTAACGCCCTCATGGTATGTGGGGTTCT
 GTATGCCACCGCTACTATGAACACCCAGACAGAAAGAGATTTTTACTATTATGACACAACACAGGGAAGAGG
 GCAAACTAGACATTGTAATGCATAAGATGCAGGAAAAAGTGCAGAGCATTAACTATAACCCCTTTGACCAGAAA
 CTTTATGCTCTATAACGATGGTTACCTCTGAATTATGATCTTTCTGTCTTGCAGAAGCCCCAGTAAAGCTGTTTA
 GGAGTTAGGGTGAAGAGAAAAATGTTTGTGAAAAATAGTCTTCTCCACTTACTTAGATATCTGCAGGGGTGT
 CTAAGAAGTGTGTTCAATTTTGAGCAATGTTTAGGTGCATAGTTCTACCACTAGAGATCTAGGACATTGTCT
 TGATTTGCTGAGTCTCTTTGGGAATCATCTGCCCTTTCAGGCGCATTTTGCAATAAAGTCTGTCTAGGTTGGGA
 TTGTCAGAGGCTAGGGGCACTGTGGGCTAGTGAAGCTACTGTGAGGAGGCTTCACTAGAAGCCTTAAATTA
 GGAATTAAGGAACCTTAAACCTCAGTATGGCGTCTAGGATCTTTGTACAGAAATATTGCCAATGACTAGTC
 CTCATCCATGTAGCACCACCTAATCTTCCATGCCGGAAGAAACCTGGGCACTTAGTTAGTAGATTAATATCT
 GGAGCTCCTCGAGGGACCAAACTCCAACCTTTTTTCCCTCACTAGCACTGGAATGATGCTTTGTATGTGG
 CAGATAAGTAAATTTGGCATCTTATATATCTACATCTGTAAGTGTGAGTTTATGGAGAGAGGCTTTTT
 ATGCATTAATTTGATCATGGCAATAAATCCAGAAGGATCTGTAGATGAGGCACCTGCTTTTTCTTTCTCTC
 ATTGCCACCTTACTAAAGTCAGTAGAATCTTCACTCATAACTTCTTCCAAAGCGAGCTCAGAGAGATTAG
 AACCACTTACTAACCAATTCACCCCCACCAACCCCTCTACTGCGTACTTTAAAAAATTAAGATTTT
 CTATGGAAGTGTCTAAGATTAGAAAAATTAATTTCTTTAATTTCAATAGACTTTAATTACATGACTCTA
 AGACTATAAGAAAACTGTAGGGAGTGAACAAAGTCTAGCAATTTATGCTATATAAAGAACTTGGAGCATA
 TGTGCAACTTATGAGTGTATCAGTTGTGCTATGAATTTTGCTTTGTTTAAAGCTGGAACCTTGAAGAAAT
 GAAATTTAATTTTTTTTCTAGGACGAGCTATAGAAAGCTATTGAGAGTATCTAGTTAATCAGTGCAGTAGT
 TGGAAACCTTGCTGGTGTATGTGATGTGCTCTCTGCTTTTGAATGACTTTATCATCTAGCTTTGTCTATT
 TCTTTGATGTTCAAGTCTCAGTCTATAGGATTGGCAGTTTAAATGCTTTTACTCCCCCTTTTAAATAAATGAT
 TAAATGTGCTTTGAAAAAATAAAAAAAAAAAAAAAAAA

FIGURE 38

MRPGLSFLLALLFFLGQAAGDLGDVGPPIPSPGFSSFPGVDSSSSFSSSSSRSGSSSSRSLGS
GGSVSQLFNSFTGSVDDRGTQCQCSVSLPDTTFPVDRVERLEFTAHVLSQKFEKELSKVREYV
QLISVYEKKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKTKLKECEASKDQNTPVVHPPTPGSCGH
GGVVNISKPSVVQLNWRGFSYLYGAWGRDYSPOHPNKGLYWVAPLNTDGRLLLEYRLYNTLD
DLLLYINARELRITYGQSGTAVYNNNMVNMVNTGNIARVNLTNTIAVTQTLNAAAYNNR
FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDDTLQVLNTWYTKQYKPSASNAF
MVCGLVYATRMTNTRTEEIFYYYDTNTGKEGKLDIVMHKMQEKVQSINYNPFDQKLYVYNDG
YLLNYDLSVLQKPQ

FIGURE 39

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAACACCCCTGTCGTCCAC
CCTCCTCCCACTCCAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGT
GGTTCAGCTCAACTGGAGAGGGTTTTCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTC
CCCAGCATCCAAACAAAGGNATGTATTGGGNGGCCCATTTGAATACAGATGGGAGACTGTTG
GAGTATTATAGACTGTACAACCCACTGGATGATTTGCTATTGTATATAAATGCTCGAGAGTT
GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACA
TGTACAACACCGGNATATTGCCAGAGTTAACCTGACC

TCTCGCAGATAGTAAATAATCTCGGAAAGGCGAGAAAGAAGCTGTCTCCATCTTGCTGTGAT
CCGCTGCTCTTGAGCTTGTTGGAGATGAGGGGAGCGCTCTGGGGCTGTGCTCCATGGCGAGCT
CGATACCATGTTGCTGGAAGTGGCCCGTCTTGCTGATGCCGATGCTGTCTAGTGGGAAC
AACTCCACTGTAACTAATGATCTATGCACTTCTGCTGTCTGGGATGTGTAGCTGTG
TGTAATGTGTGATCAGAGGTGGAAGAACAACTGAATAGATTTCTGGATTTGTGGAATG
AGAAAGGTGTGCTCTGTATATTTGTTGGCTATAAGCTGTATATCGTGTCTGCTTT
GCTTGTGCTATGTTCTATCT
CCTAGACGTCGACGTGCAACAATGGATTTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
TTATTTGGGCGATTCTCATTCGACAGCAATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
CGAGGTGCGCTTTGTTCTACCTCATACAACCTAGTCTTACTTATTTGATTTTGCACATTCATG
GAATGAATCTGCTGGTTGAAAAATGGAGAACTCAACCTCGATGTGGTATGACGCGCTTGT
TATCAGCTACAGCTCTGAATATCTCTGCTCTTTAGTCTCGATGTCTCTCTCTCTCTCTCTCT
TACACTCATCCAGCGAGTTGTTGAGAAACAGGGCTCTCATCTCTCTCTCTCTCTCTCTCTCT
CGTTGGTGCTTTCTGTAATGCTCTATAGTGCCTCAAAATCCAGAGATCTCTCTCTCTCTCTCT
TGTTACAGCTCTCAGTAATCAACAGCTTACACAATGATTTTGCATGTGTCACTATGACATC
GAACCAAAACAAATGCAACCAAGTCTACTAAGCAATTTGGCTACAAATCTACAGAGCTC
TGTCCTCAAGGAGGCGAGTCAGTCCAGTGTGGCATCTCAAGGAATATATAGGTTATCTAC
TCTTTTGTGTGGTGATTTTATCTCAGCATCCGTACTTCAACAATGACAGGTTATATAA
CTGACTCTCAACAGTGAATGATACATTAATGAAGAATGTGGAGCTAGAAGTATGATGATC
ACTGAGGATGGGGACGATGTTCCACGAGCTGTAGATAAAGAAGGATGGTGTCACTTACA
GTTATCTCTTCTTCTCATGCTTTTCTCGGCTCACTTTATATCATGATGACCTTACC
AACTGCTCCAGGTATGAACCTCTCTGTGAGATGAAAGACGTGAGCAGCTGTCTGGGTGAA
AATCTCTCCAGTGTGATTTGGCATGTGCTGTATGTTGGACACTCTGTGCCACACTTGTTC
TTACAAATGGGTGATTTGCTAGTAGAGACTCTAGCATGAAGTCCCCTTTGATTTATGCT
TTATTTGAAAAACGATATCCCAACTTTTGTAAGTTGTGTATGTTTGTCTCCCATGTAACT
TTCTCCAGTGTCTGCGCATGAATAGATTTTACTGCTGTGCTATTTGTATTTTCTTACAA
GTGCTATGATATGTAAGTAGAATGAATGCAGAGCAAGTTTTATGAATTAAGGTATGAGT
TGATAAAAGTGGCCATTATGGGCTTATCTCTGCTCTATAGTTGTGAAGTAGAGATAAA
ACAAATTTGTTGACTATTTTAAATATATATGACCTTAAGCTGTTTGTAGCACTGATTTAA
CGAAATGTATGGCTGCCTTTGAAATATTTGATGTGTTGGCGGAGGATACGCAAGAAC
ATGTTTATTTTAAATTTTAAACAAAGCTCACTTAAATGCCAGTTGTGTCATAAAATCTTAT
AGGTTTACCTTGATACGGAATTTACACAGGTAGGAGTGTGTAGTGCAACTAGTGTAGG
TTATGATGGAGGTGCGGTACATAAATGAATACGAGTAAATAATCTTACTTGGGTAGAGA
TGGCTTTGCCACAAGAGTGAAGCTGTTTGGTGTGTTTAAATCATGAAGTATGGGTCAG
GGAATGTTTGAAGCTCGAAGCTTTAGACAAGGTTTTGAAAGGATATCATGGGTTAGA
AGGAAGTGTGTTGAAGCTCACTTTGAAAGTAGTTTGGGCGCAGACGGTAGCTACCCCT
GGTATCCAGCAGCTTTGGGAGCTTAAGTGGGTAGATTCTAGGCGCCAGGAATTCAGACCA
GCTTGGCAGATGTTGAACCTGTTCTATAAAAAATATCTGCTTTGAGCATATGCTCTGTGCT
CGACACTGAGAGGCTAGTGAAGATGCTGAGGCCAGCGCAAAAGTTGCGATGACGACGATG
CTGACTGCACTCTAGCTGCGGCACAGATGAGCGCAAAAAAATATATATATTGAATACAGG
AGGCTGCTGCTGACGGGAAGGAAGTAACTGCAAAACACTAGGCTTTAGTAGGCTATAT
ATAAAATCTAGTCTGTTCTCTTTTAAAAAATGAAGACACTGAATACAGACTAAAAAT
GCTCAGATAGCTATAGGAATCTCAAGTTGGCCAAATATAGCATTTCTCTGTGACATTTAA
AAATATATTTCTATCAATATCTCAATGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
GATGTGGAATGCTGGTGTCCAGATCTCAATGTTTAACTTACACCTACTCTGTATAAATTAATGT
AGAATGAACCTGCTCTTATGATATGATACAGCTCTTCAAGAGTGTTTAAATAGCTTTGTGAT
TTACTGCCATGTAATGAAATATATAGTATTTGTGATGCTTCAACCTGAAAATCAAGCAGT
ATGAGAGTTAGTATTTGTATGTGTGCTAGTGAATGATGAGCTTTTAAAAATCAACAT
TCTTCTTTAAAAATATTTAATGTGAATGGAATATACATCTAGCTTAACTTCCCAACCT
TTATCTGTGTGATAGACATTTATTTCCCAATTTTGAATGCTCTGTCTTACCTCTATAAAT
ATGAATCTCAGAAAAAABAAAABAAAABAAAABAAAABAAAABAAAABAAAABAAAABAAAAB

FIGURE 41

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGME
EQLNKIPGFCENEKGVVPCNILVGKAVYRLCFGLAMFYLLSLLMIKVKSSSDPRAAVHNG
FWFFKFAAAIAIIIGAFFIPEGTFTTVWFYVGMAGAFCFILIQVLVLLIDFAHSWNESWVEKM
EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMLLCVGASVMSI
LPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSLLSIIGYNTTSTVPKEGQSV
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSESTLIEDGGARSDGSLEDGDDVH
RAVDNERDGVITYSYFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVVWKISSSWIGI
VLYVWTLVAPLVLTNRDFD

FIGURE 42

GCGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCCGCTGCTTCTTGNGACGTTGTGGAGAT
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC
CCGTGTTTGCTATGCCGATGCTGTCTAGTGGAAACAANTCCACTGTAAGTAGATTGATCTA
TGCACTTTTCTTGCTTGTGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAG
AACAACGAATAAGATTCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATT
TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCT
CTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGAT
TTTGGTTCTTTAAATTGCTGCAGCAATTGCAATTATTATTGGGGC

FIGURE 43

GTTATTGTGAACCTTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC
CANGTTTGTGTGGAAGTGCCCGTGTGNTATGCCGATGCTGTCCTAGTGGAACAANTCC
ACTGTAATTAGATTGATNTATGCACCTTTNTTGCTGTGTTGGAGTANGTGTAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAACCTGAATAAGATTCCTGGATTTTGTGAGAATGAGAAAG
GTGTTGTCCCTTGTAACATTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTGGTTTG
GCTANGTTCATNTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGCACAATGGATTTTGGTTTTTTAAATTTGCTGCAGCAATTGCAATTATTATTG
GGGC

AASAGCTGTCTCCAATCTTGCTGTATCCGCTGCTCTTGTAACGTTNTGGAGATGGGGAGC
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCCCCGTGTT
TGCTATGCCGATGCTGTCTAGTGGAAACAACCTCAGTAACTAGATTGATCTATGCACCT
TTCCTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAACT
GAATAAGATTCCTGGATTTTGTGAGAATGAGAAAGGTGTTGCCCTGTAAACATTTTGGTTG
GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCATTGTTCTATCTTCTCTCTTTA
CTAATGATCAAGTGAAGAGTAGCAGTAGCTTAGAGCTGCAGTGCACAATGGATTTTGGTT
CTTTAAATTTGCTGCAGCAATTGCAATTATTATTTGGGGC

FIGURE 45

GCTGTCCTTAGTGGAAACAANTCCAACCTTGTAACCTGGATTGATCTATGCACCTTTTCCTTG
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCCAGGATTGGANGAACAACTGAATA
AGATTCTCGGATTTTTGTGAGAATGAGAAAGGTGTTGTCCCCTTGTAACATTTTTGGTTGGC
TATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTCTTACT
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCT
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCCTTCATTCCAGAAGGAACCTTT
ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACTAGT
CTTACTTATTGATTTTGCACATTCATGGAATGAATCGTGGGTGAAAAATGGAAGAAGGGA
ACTCGAGATGTTGGTATGCAGCCTTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA
GTTGCTATCGTCCTGTTCTTTGTCTACTACACTCATCCAGCCAGTTGTTTCAGAAAACAAGGC
GTTTCATCAGTGTCAACATGCTCCTCTGCGTTGGTGCTTCTGTAATG

FIGURE 46

CTCGGGCGCGCAGCGAGCTCGGTTTGCCCTGCGATTGAGCTGCGGGTCGCGGCCGCGCGGCTCTCCAATT
GGCAAAATGTGTGGCTGGAGGCGAGCGAGGCTTTCGGCAAAGGCGAGTCGAGTGTTTTCGACAGCGGGCGGAG
TCCCTGTGAAGCAGATAAAAGAAACATTTATTAACGTGTCTATACGAGGGGAGCGCCGCGCGGCTGTCCGC
ACTCCCCGCGCAATTTGGCTCCCTCCAGCTCCGAGAGAGGAGAAAGAAAGCGGAAAGCGCGATTAC
GTGCTTTCCAGCAAGCTGGACCTGATCGATGGCCCTCTGAATTTATCAGATATTTGATTTATAGCAGATGCC
CCCTGGTTTGTGTGTGACGACACACAGCTGCACACAGGCTCTGGCTCGCTTCCCTCCCTCGTTTCCAGCTGCC
TCCGCGAATCCACATCTGTTTCTACCTCTCCGCGGAGGCGCAGGAGCGAGAGTGTGTGCAATCTCGGAGTG
AAGAGCGACGAGGCAAAAGAAACAAAGCCACAGACGCAACTTGAGACTCCCGCATCCCAAAAGAACGACAGAT
CAGCAAAAAAAGAAAGTGGGCCCCCCGAGCCTCTGTCTGTGCTGTCTGCTCCGCACTGTGTTCTCCCTGTGGG
TGGAAGCTCGGCCTCTCTGTGCGACACCCGCTGAAAGCGAGGTTTCAGAGGACCGCAGGAACATCCGCCCA
ACATCATCTGTGTGTGACGCGAGCAGCAGGATGTGGAGCTGGGTTCCATCGAGGTGATGAACAGACCCGCGGC
ATCATGGAGCAGGGCGGGGCGACCTTCATCAACGCTTCGTGACCACACCCATGTGCTGCCCTCAGCTCCTC
CATCTCACTGGCAAGTACGTCCACAAACACACACCTACACCAACATGAGAACTGCTCCTCGCCCTCCTGGC
AGGACAGCAGCAGAGAGCGCCACCTTTGCCGTGTACCTCAATAGCACTGGCTACCGCAGACAGCTTTCTCGGGAAG
TATCTTAATGAATACAAACGGCTCCTACGTGCCACCCGGCTGGAAGGAGTGGGTCCGACTCCTTAAAAATCCCG
CTTTTATAACTACACGCTGTGTGCGAACGGGTTGAAAGAGAACGACGGCTCCGACTCTCAAAGGATTACCTCA
CAGACCTCATACCAATGACAGCTGAGCTTCTTCGCGACGTCCTCAAGAAAGTGTACCCGACAGGCGAGTCTCT
ATGTTTCATCAGCATGACGCCCCACGGCCCTGAGGATTACGCCCCACATATTCACGCTCTTCCCAAACGC
ATCTCAGCACATCAGCGGAGCTACAACTACGCGCCCAACCCGGAACAACTGTGATCATCGCTACAGCGGGC
CCATGAAGCCCATCCACATGGAATCACCACATGCTCCAGCGGAGCGCTTCGAGACCTCATGTCCGGTGGAC
GACTCCATGGAGACGATTACAACTGCTGGTTGAGACGGGCGAGCTGGACACACCTACATCGTATACACCGC
CGACACCGTTTACCACATCGCGCAAGTTTGGCTGGTGAAGAGAAATCCATGCCATATGAGTTTGACATCGAGT
TCCCGTTTACGTGAGGGGCCCCAACGCTGGAAGCCGGCTGTCTGAATCCCCACATGCTCTCAACATTTGACCTG
GCCCCACCATCTCTGGACATTCGAGGCTGGACATACCTCGGATATGGACGGGAAATCCATCTCAAGCTGTG
GGACACGAGCGCGCGTGAATCGGTTTCACTTGAAAAAGAAAGATGAGGCTTGGCGGGACTCTCTTCTGTGTG
AGAGAGGCAAGTGCTACACAGAGAGACATGACAAAGTGGAGCGCCAGGAGGAGAACTTTGCGCCAAGTAC
CAGCGTGTGAAGGACCTGTGTACGCTGTGCTGACTACGACGCGGCTGTGAGCAGCTGGGACGAAGTGGCAGT
TGTGGAGGACGCCACGGGGAAGCTGAAGCTGCATAAGTGCAGGCGCCCATCGGCTGGCGGCGCACAGAGCC
TCTCGACCTCTGTGCCAAGTACTACGGCGAGGCGAGCGCTGCACCTGTGACAGCGGGGACATCAAGCTC
AGCTTGGCCGAGCGCCGAAAAAACTTTCAAGAAAGAGTACAAGGCCACTTCTCCGAGTCCGCTCACTCCG
CTCAGTGGCCATCGAGTGGACGCGCAGGCTGACACCTAGCGCTGGGTGATGCCGCCAGCGCAACCTCA
CCAAGCGCACTGGCCAGGCGGCTTGGAGGCAAGATGACAAAGATGGTGGGACTTCAGTGGCACTGTGAGGC
CTTCCGACTTCACTGCGCGCAACCCCATTAAGTGACACATCGGTGCTACATCTCTAGAGAACGACACAGTCCA
GTGTGACTGAGCTTACCAAGTCCCTGCGAGCTGGAAGACCAAGCTGCATCGACACGAGATTGAA
CCCTGCAGAAACAAATTAAGAACTGAGGGAAGTCCGAGGTCACTGAAGAAAAAGCGGCCAGAGAATGTGAC
TGTCAAAATCAGCTACCAACCCACGACACCAAGCGCCCTCAAGCAGAGGCTCCAGTCTGCATCTCTTCAG
GAAGGGCTGCAAGAGAGGACAAAGTGTGGCTTTGCGGGGAGCAGAAAGCGCAAGAGAACTCCGAGAGCTGC
TCAAGCGCTGCAAGAACGACGACGCTGCAGCATGCCAGGCTCAGCTGCTCCACCCACGACACCCAGCTGG
CAGACGGCGCTTTTSGACACTGGGGCTTTCTGTGCTGACCCAGCGCAACATTAACAGCTAGCTGGTGCAT
GAGGACCATCAATGAGCTCAATTTCTCTGTGAAATTTGCAACTGGCTTCTTAGAGTACTTTGATCTCA
ACACAGACCTTACAGCTGATGAATGCAGTGAACACATGGACAGGATGTCTTCAACGCTACAGTACAG
CTCATGTGAGCTGAGGAGCTGCAAGGTTTACAGCAGTGTAAACCCCGGACTGGAACATGAGCTGGATGGAG
AAGCTTTGACGATACAGCGCATTTCAGCTGCAAGAGTGGCGAGAAATGAAGACCTTCTTCCAAATCACTGG
GACACTGTGGGAGGCTGGGAAGTTTAAAGAAACACAGAGTGGACCTCCAAAACATAGAGGATCACTCGTA
CTGCAGGCAATGAAAACCATGTGGGTGATTTCCAGCAGACTGTGCTATTTGGCCAGAGGCTGAGAAAGC
AAGCAGGCACTCTCAGTCAACATGACAGATTCTGGAGGATAACAGCAGGAGCAGAGATTAAGTTCAGGAAGTCC
ATTTTTCGCCCTGTTTGTGTTGTATTATACCTCACCAGCTGCACAAATGCATTTTTCGTATCAAAAGTCC
ACCATTAACCTTCCCCAGAGCTCACAAAGGAAACGGAGAGAGCAGCAGAGAGATTTCTCTGAAATTTTC
TCCCAAGGGCGAAAGTCAATTGAAATTTTAAATCATAGGGGAAAGCAGTCTGTCTTAAATCTCTTATTCCT
TTGTTTGTCAACAAAGAGGAATCAGAAGCAGGACAGAGGCAACCTGGAGAGGCTGAAACACGTGCAGAGACG
TTTGACAAATGAGTCAGTACCAAAAGAGATGACATTTACCTAGCACTATAAACCTGGTTGCGCTGGAAGAA
CTGCCCTCAATTGTATATATGTGACTATTTACATGTATCAACTGGGAACCTTTTGGGGAACCTAATAAGAAAT
CCCAATTTTCAGGAGTGGTGGTCAATAAACGCTCTGTGCGAGTGTAAAAGAAAA

FIGURE 47

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQDRRNIRPNIILVLTDQDVELGSMQ
VMNKTRRIMEQGGAHFINAFVTTPMCCPSRSSILTGYVHNHNTYTNNENCSSPSWQAQHE
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSD
YSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFNPASQHITP
SYNYAPNPKHWIMRYTGPMKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT
YIVYTADHGYHIGQFGLVKGKSMPYEFDIRVPFYVRGPNVEAGCLNPHIVLNIDLAPTILDI
AGLDIPADMKGKSIKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEEN
FLPKYQVRVKDLCQRAEYQTACEQLGQKWQCVEDATGKLLHKCKGPMRLGSSRALSNLVPKY
YGGGSEACTCDSGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSVAIEVDGRVYHVGLGDAQ
PRNLTKRHWPGAPEDQDDKDGGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDDL DYKS
LQAWKDHKLHIDHEIETLQNKIKNLREVRGHLKKKRPEECDCHKISYHTQHKGRLKHRGSSL
HPFRKGLQEKDKVWLLREQKRKKLRLKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLG
PFCACTSANNNTYWCMTINETHNFLFCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL
HVQLMELRSCCKGYKQCNPRTRNMDLDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

FIGURE 48

AACAAAGTTCACTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA
GCTGCTGGGCAGAGAGGGACTGTCCGGCTCCCAGATGCTGGGCCTCCTGGGGAGCACAGCCC
TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCTCTGCTGCTGCTGCTGCTGCTGGCCACC
TGCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGGAAA
CCGAGTCCGCCGGGCCAGCCTTGGCCCTTCCGGCGGCGGGGCCACCTGGGAATCTTTCACC
ATCACCGTCATCTTGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCAC
CCCCGCCACACCCCTCACCACCTCCACCACCACCACCACCCCCACCGCCACCATCCCCGCCA
CGCTCGCTTGAGGCTGCTGTGCGCGGTGCCTGTGGACAGCAGCTGCCCTGCCCTCCCATCTG
TTCCCAGGACAAGTGGACCCCATGTTTCCATGTGGAAGGATGCATCTCTGGGGTGAACGAGG
GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTGTCATGGCATGCCCCAGTGTACTATGGC
AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGTCTGAAGGGTTTGGGGAGTGGAGAGCAAGG
GTGCTCTTTTCGGGGCTGGACAGCCCGTCTTGTGACAGTGACTCCCAGTGAGCCCCAGAAATG
ACAAGCGTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC
ATCAGGCTGCTGCAGGCCCTCTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCCTTTT
GGTTTGGAGAAGGCAGTGTGAGGCTGCACAGTCAATTATCGGTGCCTTAGTCCAAGAAAAAT
AAAAACCACTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 50

GCGGCTGCTGAGCTGCCTTGAGGTGCAGTGTGGGGATCCAGAGCC**ATG**TCGGACCTGCTA
 CTACTGGGCCTGATTGGGGCCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGG
 GTACTCAGGGCTACTGGCTGGGGTGGAGTGAGTGCTGGGTACCCCCCATCCGCAACGTCA
 CTGTGGCCTACAAGTTCACATGGGGCTCTATGGTGAGACTGGGCGGCTTTTCACTGAGAGC
 TGCAGCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCATGTTGGTCC
 CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC
 CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGACCCAGC
 CATGTGGTGACAGCCACCTTCCCCTACACCACCATTTCTGTCCATCTGGCTGGCTACCCGCCG
 TGTCCATCCTGCCTTGGACACCTACATCAAGGAGCGGAAGCTGTGTGCCTATCCTCGGCTGG
 AGATCTACCAGGAAGACCAGATCCATTTTCATGTGCCCACTGGCACGGCAGGGAGACTTCTAT
 GTGCCTGAGATGAAGGAGACAGAGTGGAATGGCGGGGGCTTGTGGAGGCCATTGACACCCA
 GGTGGATGGCAGAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGAAGTGAGCC
 CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTACCTGGGGCAGCAGCCGTGGCTGGGAT
 GACGGTGACACCCGAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGA
 GGAGCTGGACTTGGAGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCTGGGACTGAGC
 CCCTGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCTGAGAAGGGCAAGGAG**TAA**CCC
 ATGGCCTGCACCTCCTGCAGTGCAGTTGCTGAGGAACTGAGCAGACTCTCCAGCAGACTCT
 CCAGCCCTCTTCCTCCTTCCTCTGGGGGAGGAGGGGTTCCTGAGGGACCTGACTTCCCCTGC
 TCCAGGCCTCTTGCTAAGCCTTCTCCTCACTGCCCTTTAGGCTCCCAGGGCCAGAGGAGCCA
 GGGACTATTTTCTGCACCAGCCCCAGGGCTGCCGCCCTGTTGTGCTTTTTTTCAGACTC
 ACAGTGAGGACTTCCAGGACCCAGAATAAGCCAATGATTTACTTGTTCACCTGGAACAAAAA
 AAAAAAAAAA

FIGURE 51

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGLYGETGR
LFTESCSISPILRSIAVYYDNPHMVPPDKCRCAVGSILSEGEESPSPELIDLYQKFGFKVFS
FPAPSHVVTATFPYTTILSIWLATRRVHPALDTYIKERKLCAYPRLEIYQEDQIHFMCPILAR
QGDFYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVPGSRETSAAATLSPGAS
SRGWDDGDTRSEHSYSESGASGSSFEELDLEGEGLGESRLDPGTEPLGTTKWLWEPTAPEK
GKE

FIGURE 52

CCGCGGGAACGCTGTCTCTGGCTGCCGCCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCT
GCCCCGCGCCAGT**CAT**GACCCCTGCGCCCCCTACTCCTCCCGCTCCATCTGCTGCTGCTGCT
GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA
CCCTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGA
GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT
GACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA
GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTTGGCCTAT
GGAAAACGGGGATTTCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT
GATTGCACTAATCCGAGCCAATACTGGCTAAAGCTGGTGAAGGGCATTTCCTCTGGTAG
GGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAAT
AGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAA**TA**
ATAAATAATAAATTTTAAAAAACTTAAAAAAAAAAAAAAAAAAAA

[illegible]

MTLRPSLLPLHLLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFGDTLHI
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLLDMCVGEKRRAIIPSHLAYGKRGF
PPSPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMPALLGLIGYHLYRKANRPKVS
KKKLKEEKRNKSKKK

FIGURE 54

CCCGGGAACGTGTTCTTGGCTGCCGCACCCGAACAGCCTGTCTTGGTGCCCGGCTCCCTGC
CCCGCGCCAGTCATGACCTGCGCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGC
TGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC
CTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGAGA
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA
CCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTTGGCCTATGG
AAAACGGGGATTTCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA
TTGCACATAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAGGG
ATGGCCATGGTGCCACCCCTCTGGGCCTCATTTGGGTATCACCTATACAGAAAGGCCAATAGA
CCCAAAGTCTCCAAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA
AATAATAAATTTTAAAAAACTTA

FIGURE 55

CCGAAAGTCCCGTCCGGACCCCTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCC
GAGCCCCTGCTTTTGGAGACACGCTTCACATACACTACACGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGAAAAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGG
GCATTTTGCCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCAAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAGAAATAATAAATAATAAATTTTAAAAAACTTAAAA

FIGURE 56

CTGCTGCATCCGGGTGCTCTGGAGGCTGTGGCCGTTTTGTTTTCTTGCTGCTAAAAATCGGGGGAG
TGAGGCCGGGCCGGCGCGGCGACACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTG
ACCTGAAAAAAATGCTCTGGATTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG
GAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGAT
TATCATAGATGCAGCTGTTATTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCT
GTGGTGTATAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGA
GGTGATAGTTACAGTGAAGGTTGCTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGG
TTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTG
CTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATCTTT
TTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGACTTATGGCAGTGAACACATCTGAT
TTCCCACAGCACAAACAGCCCTGCATGGGTTGTTGTTTTTTTACTGCTCACTCCCAACCTT
TTGTAATGCCATTTTCTAAACTTATTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT
AAAATCACGAGAACACCTAAACAACAACCAAAAATCTATTGTGGTATGCATTGATTAACTT
ATAAAATGTTAGAGAACTTTCACATGAATAATTTTGTCAAATTTTATCATGGTATAATT
TGTA AAAATAAAAAGAAATTACAAAAGAAATTATGGATTTGTCAATGTAAGTATTTGTCATA
TCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGTGTTTATTCAAATGTGGT
CTCTTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTTAGTTTTTAAAAATATTCCGTGG
TCAAAATTTCTCTCACTATAATTGGTATTTACTTTTACCAAAAATCTGTGAACATGTAAT
GTAACCTGGCTTTTGAGGGTCTCCCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCAT
GGTCCAGCCACCAGGCTCCCTGTGTCCTTCCATGGGAAGGTCTTCCGTGTGCGCTCTCATT
CCAAGGGCAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC
CACATCCACCACTG

57/330

FIGURE 57

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWIIIDA AVIYPTMKDFNHSYHACGVI
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKEK
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

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FIGURE 58

TTCTTGGCTAAAATCGGGGAGTGAGGCGGGCCGGCGCGCGACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAAATGTCTGGATTTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGATC
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGAT
TTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGC
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGTTGTCTGGGTCAAACAGGTG
CTCGCATTTGGCTTTTCGTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGG
ATTCTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATT
TTCCAGAATGCCTTCATCTTTTGGAGGGCTGGTTTTTAAGTTGGC

FIGURE 59

TGGACGGACCTGAAAAAATGTTTGGATTNTAGAGGGNTTGAGATGTTTCAGAATGCATGAC
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG
GTGGATTATCATAGATGCAGNTGTATTTATCCCACCATGAAAGATTTCACCANTCATACC
ATGCCTGTGGTGTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTTGGGTCAAACAGGTGCTCGCATTTGGCTTTT
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTT
ATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGNTGTATTTTTCCAGAATGCCTTC
ATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGANTTATGCCAGTG

FIGURE 60

GGACACCGGGTCCGGACCAATGCANGACGGGGTGGANTGACCTGAAAAAATGTTTGGATT
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT
CCATTGCTGCTGGTGTAATAATTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT
TATCCCACCATGAAAGATTTNAACCACTCATACCATGCCTGTGGTGTTATAGCAACCATAGC
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
GTTTGGGTCAAACAGGTGNTCGCATTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATTT
CTGATTGNATTCTATGCGGATTCTTCTTGGAGGTATGTTGCTAAAGAAAAAGACATAGTAT
ACCCTGGAATTNCTNTATTTTTCCAGAATGCC

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FIGURE 61

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCGTGGGTGTTATAGCAACCATAGCC
TTCCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTTGGGTCAAACAGGTGNTNGCATTTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

61/330
ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCGTGGGTGTTATAGCAACCATAGCC
TTCCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTTGGGTCAAACAGGTGNTNGCATTTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

FIGURE 62

GGGAGGCTGTGNCCGTTTTGTTTTNTTGGCTAAAATCGGGGGAGTGAGGCGGCCCGGCGCGG
CGNGACACCGGGTTCCGGGAACCATTGCACGACGGGGTGGACTGACCTGAAAAAATGTTTG
GATTTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATACTATT
GCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT
TATTTATCCCACCATGAAAGATTCAACCCTCATACCATGCCTGTGGTGTATAGCAACCA
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA
GGTTGTCTGGGTCAAACAGGTGCTCGCATTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGG
ATNTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG
TATACCCTGGAATTGCTGTATTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

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FIGURE 63

CGACGCCGGCGTGA**ATG**TGGCTTCGCTGGTGTGCTGCTCTGGCTGTGCTGCTGCTGGCCGTCC
TCTGCAAGATTACTTGGGACTATTCTCTGGCAGCTCCCCGAATCCTTTCTCCGAAGATGTC
AAACGCCGCCAGCCGCTTGGTAACCTGACAAGGAGGCCAGGAAGAAGGTTCTCAAACAAGC
TTTTCTAGCCAAACCAAGTCCGCCGAGAAGCTGGATGTGGTGGTAAATGGCAGTGGCTTTGGGG
GCCCTGGTGTGAGTCTAGCTTAAAGCTGGCAAGCGAGTCTGGTGTCTGGAAACAACAT
ACCAAGGACAGGGGGGTGCTGTCTACCTTTTGGAAAGAAATGGCCTTGAATTTGACACAGGAAT
CCATTACATTGGGCGTATGGAAGAGGGCAGCATTGGCCGTTTATCTTGGCCAGATCACTG
AAGGGCAGCTGGACTGGGCTCCCTGTCTCTCTCTTTGACATCATGGTACTGGAAGGGCCC
AATGGCCGAAAGGATACCCCATGTACAGTGGAGAGAAGCCTACATTCCGGCCCTCAAGGA
GAAGTTTCCACAGGAGGAGCTATCATTTGACAAGTATATAAAGCTGGTTAAGTGGTATCCA
GTGGAGCCCCCTCATGCCATCCTGTTGAAATTCCTCCCATTTGCCGTGGTTCAGCTCCTCGAC
AGGTGTGGGCTGCTGACTCGTTTCTCTCCATTCTCTCAAGCATCCACCCAGAGCCTGGCTGA
GGTCTGTGACGAGCTGGGGGCCCTCCTGTAGCTCCAGGCAGTACGACTACATCTATCTCCCA
CTTACGGTGTCAACCCCAACACAGTGCCTTTTCCATGCACGCCCTGTGGTCAACCACTAC
ATGAAGAGGAGGCTTTATCCCGAGGGGGTCCAGTGAATTCCTTCCACACCATCCTCTGT
GATTTCAGCGGGCTGGGGGCCGTGTCTCTCAAAAGGCCACTGTGCAGAGTGTGTGTGCTGGACT
CAGCTGGGAAAGCCTGTGGTGTGTCAGTGTGAAGAAGGGCATGAGCTGGTGAACATCTATTGC
CCCATCGTGGTCTTCCAACGCAAGGACTGTTCAACACCTATGAACACCTACTGCCGGGGAAACGC
CCGCTGCTGTCCAGGTGTGAAGCAGCAACTGGGGACGGTGGCGGCCGGCTTAGGCATGACCT
CTGTTTTCTATCTGCTGCGAGGCACCAAGGAAGACCTGCATCTGCCCTCCACCAACTACTAT
GTTTACTATGACACGGACATGGACCAGGCCATGGAGGCCTAGCTCTCCATGCCCAGGGAAGA
GGCTGCCGAACACATCCCTCTTCTCTTCTTCTGCTTTCCCATCAGCCAAAGATCCGAGCTGGG
AGGACCGATTCCAGGCCGGTCCACCATGATCATGTACATACCCACTGGAGGCGAAGGTGGT
GAGGAGTGGCAGGCGGAGCTGAAGGGAAAGCGGGGCAGTGAATGAGACCTTCAAAAACTC
CTTTGCGAAGCCTCTATGTCTAGTGGTCTTGAACCTGTTCCCAAGCTGGAGGGGAAGGTGG
AGAGTGTGACTGCAGGATCCCCACTCACCACCAAGTCTTATCTGGCTGTCTCCCGAGGTGCC
GGGCGCTGCAAGGTCGCTGCTGTGACGACAGCGCCATCCTGAAGCGGAACTTGTACTCAGAC
CTTAAGAATCTTGATTCTAGGATCCGGGCACAGAAAGAAAAGAA**TAG**TTCATCAGGGAGG
AGTCAGAGGAATTTGCCAATGGCTGGGGCATCTCCCTTGACTTACCCATAATGTCTTTCTG
CATTAGTTCCTTGACGATAAAGCACTCTAATTTGGTTCTGATGCCCTGAAGAGAGGCCCTAG
TTTAAATCACAATTCGGAATCTGGGGCAATGGAATCACTGCTTCCAGTGGGGCAGGTGAGA
TCTTTACGCCCTTTTATAACATGCCATCCCTACTAATAGGATATTGACTTGGATAGCTTGATG
TCTCATGACGAGCGCGCTCTGCATCCCTCACCATGCCTCTCTAATCAGTGATCAAGGCGA
ATATTCCATCTGTGGATAGAACCCCTGGCAGTGTGTGACGTCAACCTGGTGGGTTCAGTTT
TGTCTGTAGGCTTCTGCTCTCATTTAGTGCTACGCTGCACAGTTCTACACTGTCAAGG
GAAAAGGGAGACTAATGAGGCTTAACTCAAACCTGGGCGTGGTTTTGGTTGCCATTCCATA
GGTTTTGGAGAGCTCTAGATCTCTTTTGTGCTGGGTTCTAGTGGCTCTTCAGGGGACAGGAAT
GCCCTGTGTCTGGCCAGTGTGGTCTGGAGCTTTGGGGTAACAGCAGGATCCATCAGTTAGTA
GGGTGATGTGCAGATGATCATATCCAATTCATGTGAAGTCCCGGGTCTGTCTTCTCTATCA
TCGGGGTGGCAGCTGGTTCTCAATGTGCCAGCAGGGACTCAGTACCTGAGCCTCAATCAAGC
CTTATCCACCAAATACACAGGGAAGGGTGATGCAGGGAAGGGTGACATCAGGAGTCAGGCA
TGGACTGGTAAAGATGAATACCTTTGCTGGGCTGAAGCAGGCTGCAGGGCATTCAGCCAAAGGG
CACAGCAGGGGACAGTGCAGGGAGGTGTGGGGTAAGGGGAGGAAGTGCATCAAGAAAGGGA
AAGCCACGGAAATGTGTGAAGCCCAAGAAATGGCATTGTGCAGTTAATTAGCATGTGAGGG
TTAGCAGGTAGGTGGAATGCAAGCTCAAGGTTTGGAAAAATGACTTTTTCAGTTATGTCTT
GTATCAGACATACGAAAGGTCTCTTTGTAGTTCGTGTTAATGTAACATTAAATAAATTTATTG
ATTCATTGCTTTAAAAAAAAAAAAAAAAA

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FIGURE 64

MWLPLVLLLLAVLLLLAVLCKVYLGLFSGSSPNPFSEDVKRPPAPLVTDKEARKKVLKQAFSAN
QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNLEFDTGIHYIG
RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPQ
EEAIIIDKYIKLVKVSSGAPHAILLKFLPLPVVQLLDRCGLLTRFSPFLQASTQSLAEVLQQ
LGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGGSSEIAFHTIPVIQRA
GGAVLTKATVQSVLLDSAGKACGVSVKKGHELVNIYCPIVVSNAGLFNTYEHLLPGNARCLP
GVKQQLGTVRPGGMTSVFICLRGTKEDLHLPSTNYYVYDMDQAMERYVSMFREEAAEH
IPLFFAFPSAKDPTWEDRFPGRSTMIMLIPTAYEWFEWQAEKKGKRGSDYETFKN SFVEA
SMSVVLKLPQLEGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGR LHPCVMASLRAQSPI
PNLYLTGQDIFTCGLVGALQGALLCSSLKRNLYSDLKNLDSRIRAQKKKN

[illegible]

FIGURE 66

MRVRIGLTLLLCVLLSLASASSDEEGSQDESLSKTTLTSDSVKDHTTAGRVVAGQIFLD
SESESELESSIQEEDSLKSQEGESVTEDISFLESFNPENKDYEEPKKVRKPALTAIEGTAHG
EPCHFPPFLFDKEYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEEAARRQMGEAEMM
YQTGMKILNGSNKKSQKREAYRYLQKAASMNHTKALERVSYALLFGDYLPQNIQAAREMFEK
LTEEGSPKGQTALGFLYASGLGVNSSQAKALVYYTFGALGGNLIAMVIVSRL

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FIGURE 67

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT
GCCTCCCTGCCTCTGGCCATGGCCTGCCGGTGCCTCAGCTTCTTCTGATGGGGACCTTCCT
GTCAGTTTCCCAGACAGTCTTGCCCCAGCTGGATGCAC TGCTGGTCTTCCCAGGCCAAGTGG
CTCAACTCTCCTGCACGCTCAGCCCCAGCACGTCAACATCAGGGACTACGGTGTGTCTTGG
TACCAGCAGCGGGCAGGCAGTGGCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA
CCACCGGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCACAATGCCT
GTGTCTCACCATTAGTCCCGTGCAGCCTGAAGACGACGGGATTACTACTGCTCTGTTGGC
TAGGGCTTTAGTCCCTAGGGGTGGGTGTGAGATGGGTGCCTCCCCTCTGCCTCCCATTCT
GCCCCTGACCTTGGGTCCCTTTTAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAATGGG
TTAATAATATTCAACATGTCAACAAC

CONCLUSIONS

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAG
SAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTTISPVQPEDDADYYCSVGYGFSF

[illegible]

MTPSPLLLLLLPPLLLGAFFPAAAARGPPKMA DKVVPQRVARLGRTVRLQCPEVGDPPLTMT
WTKDGRTIHSWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVLDDISPGK
ESLGPDDSSSGQEDPASQQWARPRFTQPSKMRRVRIARPVGSSVRLKCVASGHPRPDITWMK
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTSRKPV
TGTHPVNTTVDFGGTTSFQCKVRS DVKVPVQWLKRVEYGAEGRHNSTIDVGQKQFVVLPTGD
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVPDPKPPGPPVASSSSA
TSLPWPVVGIPAGAVFILGTL LLWLCAQKPKCTPAPAPPLPGHRRPGTARDRSGDKDLPS
LAALSAGPVGCLCEEHGS PAAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTSHTHSHVEGKV
HQHSHYOC

[illegible]

FIGURE 72

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLESPEGWTTWFNI
DYPGGKGDYERLDAIRFYYGDRVCARPLRLEARTTDWTPAGSTGQVVHGSPEGFWCLNREQ
RPGQNCNYSYTVRFLCPPGSLRRDTERIWSPWSPWSKCSAACGQTGVQTRTRICLAEMVSLCS
EASEEGQHCMGQDCTACDLTCMPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAIIYLLTK
TPKLLTQTDSGRFRIPGLCPDGKSILKITKVKFAPIVLTMPKTSLKAATIKAEFVRAETPY
MVMNPETKARRAGQSVSLCCKATGKPRPKYFWYHNDTLLDPSLYKHESKLVLRKLQHQHAG
EYFCKAQSDAGAVKSKVAQLIVTASDETPCNVPVPEYILRLPHDCFQATNSFYDVGRCVP
KTCAGQQDNGIRCRDAVQNCGISKTEEREIQCSGYTLPTKVAKECSCQRCTETRSIVRGRV
SAADNGEPMRFGHVYMGNSRVSMGTGYKGTFTLHVPQDTERLVLTFVDRLQKFVNTTKVLPFN
KKGSAVFHEIKMLRRKEPITLEAMETNIIPLGEVVGEDPMAELEIPSRSFYRQNGEPYIGKV
KASVTFLDPNRISTATAAQDTLNFINDEGDTFPLRTYGMFSVDFRDEVTSEPLNAGKVKVHL
DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLFNL
DVPESRRCFVKVRAYSERFLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGFNGA
CVPAFCDQSPDAYSAYVLASLAGEELQAVESSPKFNPNAIGVPQPYLNKLNRYRTDHEDPR
VKKTAFAQISMAKPRPNSAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDYNTPFN
EDDPMSWTEDYLAWWPKPMEFRACYIKVKIVGPLEVNVRSRNMGGTHRRVTGKLYGIRDVRS
TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTLKVIPQGSRRASVNPMLHEYLVNHLPLAV
NNDTSEYTMLAPLDPLGHNYGIYTVTQDPRTAKEIALGRCFDGTSDGSSRIMKSNVGVALT
FNCVERQVGRQSAFYQLQSTPAQSPAAGTVQGRVPSRRQQRASRGGQRGGVVASLRFPRVA
QQPLIN

FIGURE 73

CTGCAAGTTGTTAAACGCCATAACACACAAGTATGTTAGGCTTCCACCAAAGTCTCAATATACCTGAATACGCAC
 AATATCTTAACCTCTCATATTTGGTTTGGGATCTGCTTTGAGGTCCCATCTTCATTTAAAAAAAATACAGAG
 ACCTACCTACCCGTACGCATACATACATATGTTATATATGTAACATAGACAAAGATCCGACATCATAAAGC
 AAGCTCTGCTTTAGTTTCCAAAGAAGATTACAAAGAATTTAGAGATGATTTTGTCGAAGATCCCTCGCATTCATG
 CCTCTTGGGTTACGGTTCCTCGATCTCGGATATGACGCCCTACCCCTTTGGTTTGGGGACATTATGATTTTGTGTAAGACT
 CAGATTTACACGGAAGAAGGGAAAGTTGGGATACATGGCTGCCACCCGGAATCCACGGACATGACAAATA
 TCTGAAAGTGAACCTCGATCTCCGATATTTACCTTTGGAGACCCCTCTGAGACGTTCTGTGCAATGGGCAATC
 CCTACATGTGCAATATGATGTGATGCGAGTACCCCTGAGCTGGACACACCCCTCTGAGCTGATGTTTATGATTT
 GAAGGAAGACATCCCTCCACATTTTGGCAGTCTGCCACTTTGGAAGGAGTATCCCAAGCCTCTCCAGGTTAAACAT
 CACTCTGTCTTGGAGCAAAACCATTGAGCTAACGACACATAGTTATTACCTTTGAATCTGGGCGTCCAGACC
 AAATGATCTCGGAGAAGTCTCTGATTTATGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTA
 GATGCTTTTACATGATCCTTAATCCGTGAAGGATTATCACAGCATACGGTCTTAGAAATCATTTGCACAGA
 AGAGTACTCAACGGGTATACAACAATAGCAAAATATCCACTTTGAATCAAGACAGGTTCCGCGCTTTTG
 CTGGACCTCGCCTACGCAATATGGCTTCCCTCTACGGACAGCTGGATACACCAAGAACTCAGAGATTTCTTT
 ACAGTACACAGCTGAGGATAAGGCTGTAAAGACAGCCGTTGGGGAAATATTGTAGATGAGCTACACTTGGC
 ACGCTACTTTTTACGCGATCTCAGACATAAAGGTGCGAGGAAGGTGCAAGTGAATCTCCATGCCACTGTATGTG
 TGTATGACACAGCAAAATGACATGCGAATGTGAGCAACACTACAGGTCCAGACTGTGGGAAATGCAAGAAG
 AATTATCAGGGCCGACCTTGGAGTCCAGGCTCCTATCTCCCATCCCCAAGGCACTGCAAAATACCTGTATCCC
 CAGTATTTCCAGTATTTGTTACGAATGTCTGCGACAACGAGCTCTGCACTGCCAGAACGAGGGGACGTGCCACA
 ACAAGCTGGCGTCCGTGTGCCGGCGGCATACACGGGCATCCTCTGCGAGAAGCTGCGGTGCGAGGAGGCTGGC
 AGCTGCGGCTCCGACTCTGGCGAGGGCGCGCCCCGCAACGGCACCCCGAGCGCTGCTGCTGCTGACACGCTGCT
 GGGAAACCGCCAGCCCCCTGGTGTCTAGGTTGTCACCTCCAGCCACACCGGACGGGCTGTGCGGTGGGGAAGCA
 GACACAACCCAAACATTTGCTACTAATACATAGGAACACACACATACAGACACCCCACTCAGACAGTGTACAAA
 CTAAGAAGGCCCTAACTGAACATAAGCCATATTATCACCCGTGGACAGCACATCCGAGTCAAGACTTTAAATTC
 TGACTCCAGAGGAGTTGGCAGCTGTTGATATTATCACTGCAAAATCACAATGCCAGCTCAGAGCATATTGTGGA
 TTGGAAGAAGCTGCGACAGCCCCCAACAGGAAGACAAAAACAAACAAATCAACCGACTTAAACCATTTGGC
 TACTCTAGCGTGGTGCGCCCTAGTACGACTCGGCCAGTGTGGGCAACCAATAGCATTTCTTGTGTGTCAG
 GTGCAATTTGGGCGATAAGGAATCTGTTACAAGCTGCCATATTGGCCTGCTTCGTCCTGAATCCCTTCCAC
 CTGTGCTTTAGTGAACGTTGCTCTGTAAACCTCGTTGGTTGAAAGATTCTTTGCTGATGTTAGTGATGCACA
 TGTGTAAACAGCCCCCTCTAAAGCGCAAGCCAGTATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGGCA
 GCACACACCCACTATACAAGAGTGGCTATAGGAAAAAGAAAGTGATCTATCCTTTGTATTCAAAATGAAGTT
 ATTTTTCTTGAACACTACTGTAATATGATAGTTTGTATTATTGCCAATTTGTGTACACAGCAATCTGTAAAT
 GTATCTAATTCGAATCAGCAAAAGACTGACATTTTATTTTGTCTCTTCTGCTCTGTTTGTTCACGTGTGACGA
 GATTCTCTGTGAAGGCAAGCAAGCTGCTGGCATCAAGAATATCAGTTTACATATAACAAGGTGAATAAGA
 TTCCACCAAGGACATTTCAATGTTTCTTGTGCTTTAACTCTGGAAGATTTAAAGAAATAAAACCTCGTGA
 TAAACGATTTTCAAGAAATTTGATTTGCAATTTCTTAAGATGAAGGAACAGCCACCAAGCAGTTTCCACTCACT
 TTAATGATTTCTGTGTGGACTGAGTACATTCAGCTGACGAATTTAGTTCAGGAGAGATGGATGTATGTTCACT
 AGCTTGGACAACTTCTGC AAAATATGAGACTATTTCCACTTGGGAAAAATACACAGCAAAAAA AAAAAA

FIGURE 74

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPPELMFDFEGRHPSTFWQSATWK
EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMLEKSLDYGRTWQPYQYYATDCLDAF
HMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD
TTKKLRDFFTVTDLRIRLLRPVAGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN
SKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPPIPKGTANTCIPSISSIGTNVCDNELLH
CQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSGSDSGQGAPPHGTPALLLLTTLLGTAS
PLVF

FIGURE 75

CCCACGCGTCGCGGTGACCTGGGCCGAGCCCTCCCGGTGCGCTAAGATTGCTGAGGAGGCGG
 CGGGTAGCTGGCAGGCGCCGACTTCCGAAGGCCGCGTCCGGGCGAGGTGTCCTCATGACTT
 CTCTTGTGGACCATGTCCGTGATCTTTTTTGCCTGCGTGGTACGGGTAAGGGATGGACTGCC
 CCTCTCAGCCTCTACTGATTTTTTACCACACCCAAGATTTTTTGAATGGAGGAGACGGCTCA
 AGAGTTTAGCCTTGCAGCTGGCCCAGTATCCAGGTCGAGGTTCTGCAGAAGGTTGTGACTTT
 AGTATACATTTTTCTTCTTTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC
 AGCAGCCATGGCCTTCTGCTTCTGGAGACCCCTGTGGTGGGAATTCACAGCTTCCCTATGACA
 CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTAG
 AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGCAGCTTGGAAAAAT
 TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCTGGAGGACACAGATGTGGCAA
 ATGGGGTGATGAATGGTCACACCCGATGCACTTGGAGCCTGCTCCTAATTTCCGAATGGAA
 CCAGTGACAGCCCTGGGTATCCTCTCCCTCATTCTCAACATCATGTGTGCTGCCCTGAATCT
 CATTTCGAGGAGTTCACCTTGCAGAACATTTTACAGGATCCAAGGAGCTGGTTCTGCTGGT
 TGGACCAAACCTCGTGAGCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT
 CCGGGAGCAGTGATGTCAAACCTTCTGCTGCTGGGGAATCTCATCAGCAGGAGCCTGTGGA
 AAAGGGCATGTCAGTGAAATCTGGGAATGGCTGGATTCCGAAACATCTGCCATGTGTATTG
 ATGGCAGAGCTGTTGCCACAAGCGCCTTTTATTAGGGTAAAATTAACAAATCCATTCTAT
 TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCCCTACATTTATATGATTCTGGGGTT
 GCTTCAGAAGTGTTATTTTCATGAATCATTATATGATTGATCCCCAGGATTCATTATTTGT
 TTAATGGGCTTTTCTACTAAAGCATAAATACTGAGGCTGATTTAGTCAGGGCAAAACCAT
 TTACTTTACATATTCGTTTTCAATACTTGCTGTTTCATGTTACACAAAGCTTCTTACGGTTTTTC
 TTGTAACAATAAATATTTTGTAGTAAATAATGGGTACATTTTAAACAACTCAGTAGTACAACC
 TAAACTTGTATAAAAGTGTGTAAAAATGTATAGCCATTTATATCTATGTATAAATTAATG
 AGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTTTATTAACAAAAAAAAAAAAAAAAAA
 AAAAG

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FIGURE 76

MSVIFFACVVVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFSIF
SSFGDVACMAICSCQCPAAMAFCFLET LWWEFTASYDTTCIGLASRPYAFLEFDSIIQKVW
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

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FIGURE 77

TGCTTCCTGGAGACCCTGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGCNT
AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTCAGAAAAGTGAAGTGGCATT
TTAACTATGTAAGTTCCTNTCAGATGGAGTGCAGCTTGAAAAAATTCAGGAGGAGCTCAAG
TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAAATGGGGT

0959382.11901

FIGURE 78

CTCAGCGGCGCTTCCTCGTAGCGAGCCTAGTGCGGGGTGTTTGCATTGAAACGTGAGCGCGA
 CCCGACCTTTAAAGAGTGGGGAGCAAAGGGAGGACAGAGCCCTTTAAACGAGGCGGGTGGTG
 CCTGCCCTTTTAAAGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTT
 TCTGTCCGAGGCTGCGAGGAAAGGCCCTTAGGCTGGGTCTGGGTGCTTGGCGGCGGCGGCTT
 CCTCCCCGCTCGTCTCTCCCGGGCCAGAGGCACCTCGGCTTCACTCATGCTGAGCAGAGTA
TGGAAGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGC
 GAGTGTATTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCTTGAC
 CCGCTTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGA
 TTGCGCTCGAGCTGTGCACCTTTACCTGGCAATTGCCCTGGGTGCTGTCTGCTCTCTGCC
 TTCTCCATCATCAGCAATGAGGTGCTGCTCTCCCTGCCGGAACACTACATCCAGTGGCT
 CAACGGCTCCCTCATCCATGGGCTCTGGAACCTTGTGTTTCTCTTCCCCAACCTGTCCCTCA
 TCTTCTCATGCCCTTTGCATATTTCTTCACTGAGTCTGAGGGCTTGGTGGCTCCAGAAAG
 GGTGCTCTGGGCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTCTGCTGGTGCT
 AGGTATGGTGTTGGTGCCATCAGCCATTGTGGACAAGAACAAGGCCAACAGAGAGTCACTCT
 ATGACTTTTGGGAGTACTATCTCCCTACCTCTACTCATGCATCTCCTTCTTGGGGTTCTA
 CTGCTCCTGGTGCTACTCCATGGGTCTCGCCCGCATGTTCTCCGTCACTGGGAAGCTGCT
 AGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGACAGCTGTACTGCTCAGCCTTTGAGGAGG
 CAGCCCTGACCCGAGGATCTGTAATCCTACTTCTGCTGGCTGCCCTTAGACATGGAGCTG
 CTACACAGACAGGTCTGGCTCTGCAGACACAGAGGGTCTGCTGGAGAAGAGGCGGAAGGC
 TTCAGCCTGGCAACGGAACCTGGGCTACCCCTGGCTATGCTGTGCTTGGTGGTGCTGACGG
 GCCTGTCTGTGCTCATTGTGGCCATCCACATCCTGGAGCTGCTCATCGATGAGGCTGCCATG
 CCCCAGGCATGCAGGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAGCTGGGCTCCTTTGG
 TGCCGTCACTCAGGTGTACTCATCTTTACCTAATGGTGCTCAGTTTGGGCTTCTATA
 GCTCTCCACTCTTCCGGAGCCTGCGGCCAGATGGCACGACATGCCATGACCGAGATAATT
 GGGAACTGTGCTGTCTCTGCTGCTTAAGCTCAGCACTTCTGTCTTCTCTCGAACCTGGG
 GCTCACTCGCTTTGACCTGCTGGGTGACTTTGGACGCTTCAACTGGCTGGGCAATTTCATA
 TTGTGTTCTCTACAAACGAGCCTTTGCAGGCCTCACCACACTCTGTCTGGTGAAGACCTTC
 ACTGCAGCTGTGCGGGCAGAGCTGATCCGGGCTTTGGGCTGGACAGACTGCCCTGCCGCT
 CTCGGTTTCCCCAGGCATCTAGGAAGACCCAGCACCACTGCACTCCAGCTGGGGTGGGA
 AGGAAAAAACTGGACACTGCCATCTGCTGCCTAGGCCCTGGAGGGGAAGCCCAAGGCTACTTGG
 ACCTCAGGACCTGGAATCTGAGAGGGTGGGTGGCAGAGGGGAGCAGAGCCATCTGCATATT
 GCATAATCTGAGCCAGATTTTGGGACCAGGACCTCCTGCTTTTCCATACTTAAGTGTGGCCT
 CAGCATGGGGTAGGGCTGGGTGACTGGGTCTAGCCCTGATCCCCAATCTGTTTACACATCA
 ATCTGCCTCACTGCTGTCTTGGGCCATCCCATAGCCATGTTTACATGATTTGATGTGCAAT
 AGGGTGGGGTAGGGGACGGGAAAGGACTGGGCCAGGGCAGGCTCGGGAGATAGATTGTCTCC
 CTTGCCCTCTGGCCCCAGCAGAGCCTAAGCACTGTGCTATCCTGGAGGGGCTTTGGGACCACTA
 AAAGACCAAGGGGATAGGGAGGAGGAGGCTTCAGCCATCAGCAATAAAGTTGATCCAGGGA
 AAAAAA

FIGURE 79

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATVNK
IALELCTFTLAIALGAVLLLPFSIIISNEVLLSLPRNYIIQWLNGSLIHGLWNLVFLFPNLSL
IFLMPFAYFFTESEGFAGSRKGVLG RVYETVVMLMLLTLLVLGMVWVASAIVDKNKANRESL
YDFWEYYLPYLYSCISFLGVLLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEEQLYCSAFEE
AALTRRICNPSTCWLPDLMELLHRQVLALQTORVLEKRRKASAWQRNLGYPLAMLCLLVLT
GLSVLIVAIHILELLIDEAAMPGRMQGTSLGQVSFSKLGSGFAGVIQVVLI FYLMVSSVVG FY
SSPLFRSLRPRWHD TMTQIIGNCVCLLVSSALPVFSRTLGLTRFDLLGDFGRFNWLG N FY
IVFLYNAAFAGLTTLCLVKTF TA AVRAELIRAFGLDRLPLPVSGFPQASRKTQH Q

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FIGURE 80

GGCTGCCGAGGGAAGGCCCTTGGGTTGGTCTTGGTTGCTTGGCGGCGGCGGNTTCNTCCCC
GCTCGTCCTCCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGTGTA
TTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTC
AAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCG

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FIGURE 81

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAACGAGGCGGTGGTGC
CTGCCCTTTAAGGGCGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTTTC
TGTCGCAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGTGCTTGGCGGCGGCGCTTCCT
CCCCGTTGTCNTCCCGGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCCTGACCCGC
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGTCTCTGCCCTTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

FIGURE 82

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT
GGAATTGAGGAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTTC**ATG**CTGCTGT
GGGTGATATTACTGGTCCTGGCTCCTGTCAGTGGACAGTTTGCAAGGACACCCAGGCCCAT
ATTTTCCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCTCACTTGCAA
GGGATTTTCGCTTCTACTCACCACAGAAAACAAAATGGTACCATCGGTACCTTGGGAAAGAAA
TACTAAGAGAAAACCCAGACAATATCCTTGAGGTTCAGGAATCTGGAGAGTACAGATGCCAG
GCCAGGGCTCCCCCTCTCAGTAGCCCTGTGCACTTGGATTTTTCTTCAGAGATGGGATTTCC
TCATGCTGCCCAGGCTAATGTTGAACTCCTGGGCTCAAGTGATCTGCTCACC**TAG**GCCTCTC
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGAC
TCTGTGGTTCTGAGGTGCCGGGCAAGGCCGAAGTAACACTGAATAATACTATTACAAGAA
TGATAATGTCCTGGCATTCTTAATAAAAGAACTGACTTCCAAAAAAAAAAAAAAAAAAAAA
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FIGURE 84

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCGCGCCCCCGGTGT
 GAGGCGGCCTCACAGGGCCGGTGGGCTGGCGAGCCGACGCGGCGGGAGGAGGCTGTGAG
 GAGTGTGTGGAACAGGACCCGGGACAGAGGAAC**CAT**GGCTCCGCAGAACCTGAGCACCTTTT
 GCCTGTTGCTGCTATACCTCATCGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTG
 GGGGTGCCCTCGAAGTGCCTCTATAAAGGATATTAAAAAGGCCTATAGGAACTAGCCCTGCA
 GCTTCATCCCGACCCGAACCTGATGATCCACAAGCCCAGGAGAAATTCCAGGATCTGGGTG
 CTGCTTATGAGGTTCTGTGAGATAGTGAGAAACGGAAACAGTACGATACTTATGGTGAAGAA
 GGATTAAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTACACTTCTTTGGGGATTT
 TGGTTTCATGTTTGAGGAACCCCTCGTCAGCAAGACAGAAATATCCAAGAGGAAGTGATA
 TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTT
 AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTGCGCAAGAGAT
 GCGGACCACCCAGCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT
 GCCCTAATGTCAAAGTAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTG
 AGAGACGGCATGGAGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG
 AGATTTACGGTTCCGAATCAAAGTTGTCAAGCACCCAAATATTTGAAAGGAGAGGAGATGATT
 TGTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT
 CACTTGGATGGTCACAAGGTACATATTTCCCGGGATAAGATCACCAGGCCAGGAGCGAAGCT
 ATGGAAGAAAGGGGAAGGGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAA
 TCACCTTTTGATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAA
 CAGCTACTGAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATAT**TGAG**AGTG
 AATAAAATTGGACTTTGTTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGTTTTT
 TTGTGTGTGTTTTGTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTATCTAATGA
 TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTGCAATCGGAAAAGAATGACC
 AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGTGCCGCTGAGT
 TTCAAGAATTAAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGTTGGA
 GTTGTTAGCAATTTCAATCAAATGCCAACTGGAGAAGTCTGTTTTTAAATACATTTTGTG
 TTATTTT

FIGURE 85

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKLALQLHPDRNPDDPQ
AQEKFQDLGAAYEVLSDSEKRRKYDITYGEEGLKDGHQSSHGDI FSHFFGDFGFMFGGTFRQQ
DRNIPRGSDIIVDLEVTLEEYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ
MTQEVVCDCEPNVKLVNEERTLEVEIEPGVRDGMIEYFFIGEGEPHVDGEPGDLRFRIVVKH
PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVVHISRDKITRPGAKLWKKGEGLPNFD
NNNIKGSIIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

FIGURE 86

TGGGACCAGGGAACCCCGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA
GCGGCGGGCGGAGGAGGTTTTGAGGATTTTGGAACAGGACCCGGACAGAGGAACCATGGTT
CCGCAGAACNTGAGCACNTTTTGCTGTTGNTGNTATACTTCATCGGGCGGTGATTGCCGG
ACGAGATTTNTATAAGATTTTGGGGTGCCTNGAAGTGCCTTNTATAAAGGATATTAAAAAGG
CCTATAGGAACTAGCCCTGCAGNTTTATCCCGACCGGAACCCTGATGATCCACAAGCCCAG
GAGAAATTCAGGATTTGGGTGCTGCTTATGAGGTTNTGTGAGATAGTGAGAAACGGAACA
GTACGATAATTATGGTGAAGAAGGATTAAGATGGTNATCAGAGCTCCCATGGAGACATTT
TTTCACACTTNTTGGGGATTTTGGTTTCATGTTTGGAGGAACCCCTNGTCAGCAAGACAGA
AATATTCCAAGAG

FIGURE 87

GGCACGAGGCGGCGGGGCAGTGC GCGGGATGCGCCCGGAGCCACAGCCTGAGGCCCTCAGGT
 CTCTGCAGGTGTCGTGGAGGAACCTAGCACCTGCCATCCTCTTCCCCAATTGCCACTTCCA
 GCAGCTTTAGCCCATGAGGAGGATGTGACCGGGACTGAGTCAGGAGCCCTCTGGAAG**CATGG**
 AGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCATCTTTCTGGCTTCGTTTGCAGCC
 TTGGTGCTGCTTTCAGGCGAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATTC
 TAAGCCCATTTGGACCTCATTTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC
 TGGACGATGTCGTTATCACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC
 GAAGATGCCTCGGGTCTCATGTCCCACTGCATTGCCATCTTGAAGATTGTGCACACTCTGAC
 AGAGAAGCTTGTGCCATGACAATGGGCTCTGGGGCCAAAGATGAAGACTTCAGCCAGTGTCA
 GCGACATCATTTGGTGGCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG
 TACCCTCCGTTGGACCCCAAACCTCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTCTGAG
 TCACCTGCTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCTGGACTGGATTGACC
 AGTCTCTGTGCGCTGCTGAGGAGCATTGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAG
 CCAGATAAAGGCCTCCCAGGCCCTGAAGGCTTCTCTGCAGGAGCAGTCTGCAATTT**TAGT**GCCT
 ACAGGCCAGCAGCTAGCCATGAAGGCCCTTCCCGCCATCCCTGGATGGCTCAGCTTAGCCCTT
 CTACTTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTCAGCTGTGTGTGCATAG
 TAAAGCAGGAGATCCCCGTCAGTTTATGCCTCTTTTGCAAGTTGCAAACTGTGGCTGGTGAGT
 GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACTCTCTGCAAGAGGAGTATTGAAAA
 CTGGTGGACTGTCAGCTTTATTTAGCTCACCTAGTGTGTTTCAAGAAAAATTGAGCCACCGTCT
 AAGAAATCAAGAGGTTTCACATTAAAATTAGAATTTCTGGCCTCTCTCGATCGGTGAGAATG
 TGTGGCAATTTCTGATCTGCATTTTTCAGAAGAGGACAATCAATTGAAACTAAGTAGGGGTTTC
 TTCTTTTGGCAAGACTTGTACTCTCTCACCTGGCCTGTTTCATTTATTTGTATTATCTGCCT
 GGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGCAAGTTTGGGTTTGAAGCTGAGGAAC
 ACAAGTTGATGATTTCTTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTG
 GATAGTAAATTTATACTTATGTTTCCCTCAAAAAAAAAAAAAA

88/330

FIGURE 88

METVVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSEL
ELDDVVITNPHIEAILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKTAS
VSDIIVVAKRISPRVDDVVKSMYPPLDPKLLDARTTALLSVSHLVLTRNACHLTGGLDWI
DQSLSAAEHLEVLREAALASEPDKGLPGPEGFLQEQSAI

FIGURE 89

GCTTCATTTCTCCCGACTCAGCTTCCCACCCTGGGCTTTCCGAGGTGCTTTCGCCGCTGTCC
CCACCACTGCAGCCATGATCTCCTTAACGGACACGCAGAAAAATTGGAATGGGATTAACAGGA
TTTGGAGTGTTCCTGTTCTTTGGAATGATTCTCTTTTGGACAAAGCACTACTGGCTAT
TGGAATGTTTTATTTGTAGCCGGCTTGGCTTTTGTAAATGGTTTAGAAAGAACATTCAGAT
CTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTCTGGGTGGTGTATTGTAGTC
CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTCTCTTGTTCAG
GGGCTTCTTCCTGTCGTTGTTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT
TTACCTGGAATTAGATCATTGTAGATAAAGTTGGAGAAAGCAACAATATGGTATTAACAACA
AGTGAATTTGAAGACTCATTTAAATATTTGTGTTATTTATAAAGTCATTTGAAGAATATTCA
GCACAAATTAATATTACATGAAATAGCTTGTAAATGTTCTTTACAGGAGTTTAAACGTATAG
CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAACAGGCTTCTACTCAAGTGA
ACTAAGAAGAAGTCAGCAAGCAAACTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA
ACTCTGAAGGCTATTTGTGTTGTTTTCCACAATGTGCGAACTCAGCCATCCTTAGAGAA
CTGTGGTGCCTGTTCTTTCTTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCT
TTTLAGAAGTGTCCACTGCAATGGCAAAAATATTTCCAGTTGCACTGTATCTCTGGAAGTGA
TGCATGAATTCGATTGGATTGTGTCATTTAAAGTATTAACCAAGGAACCCCAATTTTG
ATGTATGGATTACTTTTTTTGNGCNCAGGGCC

FIGURE 90

MISLTDTQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFFQK
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFTIRRVPLGSLNLNLPGI
RSFVDKVGESNNMV

Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

FIGURE 91

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTTCTCCCGACTCAGCTTCCC
ACCNTGGGCTTTCCGAGGTGCTTTCGCCGCTGTCCCCACCACTGCAGCCATGATCTCCTTAA
CGGACACGCAGAAAAATTGGAATGGGATTAACCGGATTTGGAGTGTTTTTCTGTCTTTGGA
ATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTTATTGTAGCCGGCTT
GGCTTTTGTAATTGGTTTAGAAGAACATTCAGATTCTTCTTCCAAAAACATAAAATGAAAG
CTACAGGTTTTTTCTGGGTGGTGATTTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATG
ATCTTCGAAATTTATGGATTTTTTCTCTTGTTT

FIGURE 92

GGCACGAGGCTGAACCCAGCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAA
 GGCTGCCAGGAAGGAGACGCCCTTCTGAGTCTTGATCTTTCTTCCCTCTGGAAATCTTTGA
 CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATCATGGACCTCGCGGACTGC
 TGAAGTCTCAGTTCCTGTGCCACCTGGTCTTCTGTACGTCTTTATTGCCCTCAGGGCTAATC
 ATCAACACCATTTCAGTCTTCACTCTCCTCCTCTGGCCCATTAACAAGCAGCTCTTCGGAA
 GATCAACTGCAGACTGTCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT
 CGGGCACGGAATGCACCATCTTCACGGACCCGCGCGCTACCTCAAGTATGGGAAGGAAAAAT
 GCCATCGTGGTTCTCAACCACAAGTTTGAAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGA
 ACGCTTTGGGCTGTAGGGGGCTCCAAGGCTCTGGCCAAGAAAGAGCTGGCCTATGTCCCAA
 TTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTTCGCGCAAGTGGGAGCAGGAT
 CGCAAGACGGTTGCCACAGTTTGCAGCACCTCCGGGACTACCCGAGAAGTATTTTTTCTCT
 GATTCAGTGTGAGGGCACACGGTTACGGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCC
 GGGCCAAGGGGCTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATC
 ACCGTGAGGAGCTTGAGAAATGTAGTTTCAGCTGTATATGACTGTACACTCAATTTTCAGAAA
 TAATGAAAATCCAACACTGCTGGGAGTCTTAAACGGAAGAAATACCATGCAGATTTGTATG
 TTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCCTGGCTGCAC
 AAGCTCTACCAGGAGAAGGATGCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCCAGA
 GACGCCCATGGTGCCCCCGGCGGCCCTGGACCTCGTGAACCTGGCTGTTTTGGGCCCTCGC
 TGGTGCTCTACCCCTTCTTCCAGTTCTCTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACG
 CTGGCCAGCTTCATCCTCGTCTTCTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGT
 GACGGAATTTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACT
GACTCAGGAGGTGTACCATCCGAAGGGAACCTTGGGGAACCTGGTGGCCTCTGCATATCCT
 CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCCCTGTGGGCACGGCGGAAGTACGA
 CCTCTCCAGCCAGGAGTCTGGTCTCAAGGCCGATGGGGAGGAAGATGTTTTGTAATCTTT
 TTTTCCCCATGTGCTTTAGTGGGCTTGGTTTTCTTTTTGTGCGAGTGTGTGTGAGAATGGC
 TGTGTGGTGAGTGTGAACTTTGTCTGTGATCATAGAAAGGATATTTTAGGCTCGAGGGGAG
 GGCAGGGCTGGGGACCGAAGGGGACAAGTTCCCTTTTCATCCTTTGGTGCTGAGTTTTCTGT
 AACCCTTGGTGTGCCAGAGATAAAGTGAAAAGTGCTTTAGGTGAGATGACTAAATATAGCCTC
 CAAGAAAAAAAATTAAGTGCTTTTCTGGGTCAAAAAAAAAA

FIGURE 93

MDLAGLLKSQFLCHLVFCYVFIASGLIINTIQLFTLLLWFPINKQLFRKINCRLSYCISSQLV
MLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHKFEIDFLCGWSLSERFGLLGSKVLAKK
ELAYVPIIGWMWYFTEMVFCSRKWEQDRKTVATSLQHLDYPEKYFFLIHCEGTRFTEKKHE
ISMQVARAKGLPRLKHLLPRTKGFALTVRSLRNVSAVYDCTLNFRNNENPTLLGVLNGKK
YHADLYVRRIPLEIDIPEDDDECSAWLHKLYQEKDAFQEEYYRTGTFPETPMVPPRRPWTLVN
WLFWASLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVRRMIGVTEIDKGSAYGNSDS
KQKLND

FIGURE 94

CTGAGGCGGCGGTAGCATGAGGAGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCG
 GCGCACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTCTTCTGGGGAA
 GTAAAGGTGAAGCCAAGAACAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTA
 TACAATTGACATTAGAAAATATATTCATGCTATCAGCTTTTAGCTTTTATAATTCTTCAG
 GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTCAAATGTCAAAAAGAAATGTGGTAGGT
 TGGTACAAATTCGTCGTCATTGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAA
 AAACCTGTCAGGAGCATTTTTCAAACCAAGACCTTGTTTTTCTGCTATTAAACCAAGTATAA
 TAACGAAAGCTGCTCTACTCATCGACTGGAACATTCTTATATAAACCTCAAAAAGGACTT
 TTTCACAGGGTACCTTTAGTGGTTGCCAATCTGGGCATGTCTGAACAACTGGGTTATAAAAC
 TGTATCAGGTTCTGTATGTCCACTGGTTTTAGCCGAGCAGTACAAACACACAGCTCTAAAT
 TTTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA
 CAAGAGGAATTAAGAGTATATGCAAAAAAGTGAAGACAGTGAACAAGCAGTAGATAAACT
 AGTAAAGGATGTAACAGATTAATAACGAGAAATTGAGAAAAGGAGAGGAGCACAGATTGAGG
 CAGCAAGAGAGAAGAACATCCAAAAAGACCTCAGGAGAACATTTTCTTTGTGTCAGGCATTA
 CGGACCTTTTTCCAAATTCGTAATTTCTTCATTCATGTGTTATGTCTTTAAAAAATAGACA
 TGTTTCTAAAAGTAGCTGTAACATAACCACCATCTCGATGTAGTAGACAATCTGACCTTAA
 TGGTAGAACACACTGACATTCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAAAGCAT
 AAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTAGATACACAAGA
 CAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCC
 CAGAAAAGATGAAGAAATGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTCCTACA
 TTTTGAATCCTTTTAAACCTTACAAGGAGATTTTTTATTGGCTGATGGGTAAAGCCAACAT
 TTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCAATTTGTTTTTACTATGTTAC
 CTGTTTGCAGTAATACACAGATAAATCTTAGTGCATTTACTTCACAAAGTACTTTTTCAAAC
 ATCAGATGCTTTTATTTCAAACCTTTTTTTTCCCTTTTCTAAGTTGTTGAGGGGAAGGCT
 TACACAGACACATTCTTTAGAATTGGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAA
 TCCCAGCATTAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC
 TGGGCAACGTATTGAGACCATGTCTATTAATAAATAAATGAAAAGCAAGAATAGCCTTAT
 TTTCAAATATGGAAGAAATTTATATGAAAATTTATCTGAGTCATTAAATTTCTCCTTAAG
 TGATACTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCA
 ATAAATTTGCAAAACATCATCTAAATTTAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTT

MEGESTSAVLSGFVLGALAFQHLNLTSDSTEGFLLGEVKGAEAKNSITDSQMDDDEVVYTIDIQ
KYIPCYQLFSFYNSSGEVNEQALKKILSNVKNVVGWYKFRHSDQIMTFRERLLHKNLQEH
FSNQDLVFLLLTPSIITESCSTHRLHSLYKPKQGLFHRVPLVANLGMSEQLGKTVSGSC
MSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVN
RLKREIEKKRGAQIAAREKNIQDPQENIFLCIQALRTFFPNSEFLHSCVMSLKNRHVSKSS
CNYNHLDLVNDNLTMVEHTDIPEASFASTQYR11KKALDLDLRWQFKRSRLDQTQDKRKA
NTGSSNQDKASKMSSPTEDEIEKMGFGFEYSRPTF

FIGURE 96

GGCACAGCCGCGCGCGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGGACGAGCGGACCGAGCGCAGGGCGACG
 CCAAGCAGCGCGCAGCGAACGCGCGCGCCACACCTCTCGGGTCCCGCGCGGCGCTGCCACCCTTCCTT
 CCTTCCCCGCGTCCCCGCTCGCGCGCCAGTCAGTTTGGCGGGTTCGTCGCCCGGAAACCCCGAGGTCACCA
 GCCCGCGCTCTGCTTCCCTGGGCGCGCGCGCTCCACGCCCTCCTTCTCCCTTGGCCGCGGCGCTGGCACC
 GGGGACCGTGTGCTGACGCGGAGGCCAGCTCTACTTTTCGCCCGCGCTCTCTCCGCTGCTCGGCTCTCCAC
 CAACTCCAATCCTTCTCCCTCCAGCTCCACTCGCTAGTCCCCGACTCCGCGAGCCTCGGCGCGCTGGCGTAG
 CGCGCTTCCGCTCCGCTCCCAAAGGTGGGAACGCGTCCGCGCGCGCCGCGACCAATGCGAGGTTCCGCTTGC
 CGCGCTTCTGCGACCTGGCAGTGTCTCAGCGCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAGTTGCTCGG
 AAGTCGCGACTCTTACGTGTCCAAAGGCTTCAAAGAAGCATGCCCGCTCCACGAGATCAACGGTGATCAT
 TTGAAGATCTGTCCCGAGGTTCTACCTGCTGCTCAAGAGATGGAGGAGAAGTACAGCCTGCAAGTAAAGA
 TGATTTCAAAGTGTGGTCAGCGAACAGTGAATCATTTGCAAGCTGTCTTTGCTTACAGTTACAAGAAGTTTG
 ATGAATTTCTCAAAGAACTACTTGAAAATGCAGAGAAATCCCTGAATGATATGTTTGTGAAGACATATGGCCAT
 TTATACATGCAAAATTTCTGAGCTATTTAAAGATCTCTTCGTAGAGTTGAAACGTTACTACGTGGTGGGAAATGT
 GAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCTCCTGGAGCGGATGTTCCGCTTGGTGAATCCCACT
 ACCACTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCCT
 CGCAAAATTGAAGCTCCAGTTACTCGTGCTTTGTAGCAGCCCTACTTTCGCTCAAGGCTTAGCGGTTGCGGG
 AGATGCTGCTGAGCAAGGCTCCCGTGGTAAACCCACAGCCCACTGACCCATGCCCTGTTGAAGATGATCTACT
 GCTCCCACTGCCGGGTCTCGTGACTGTGAAGCCATGTTACAACTACTGCTCAAAACATCATGAGAGGCTGTTTG
 GCCAACCAAGGGGATCTCGATTTTGAATGGAACAAATTCATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGA
 GGGTCCCTTCAACATGAAATCGGTCATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAAG
 ATAATAGTGTTCAGTGTCTCAGAAGGTTTTCAGGGATGTGGACCCCCAAGCCCTCCCACTGGACGAAT
 TCTCGTCCATCTCTGAAAGTGCCCTCAGTGCTCGCTCAGACCACATCAGCCGAGGAGCGCCACACAGC
 AGCTGGCACTAGTTTGGACCGACTGGTTACTGATGTCAAGGAGAACTGAAACAGGCAAGAAATTTGGTCTCT
 CCCTTCCGAGCAACGTTTGGCAACGATGAGAGGATGGCTGAGGAAACGGCAATGAGGATGACTTGTGAATGGG
 AAAGGCAAAAGCAGGTACTGTTTGCAGTGACAGGAAATGGAATAGCCAAACAGGCAACACACAGAGGTTCCA
 GGTGTGACACCAAGCAACAGACATACTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGA
 AGAATGCATCAATGGGAACGACGTGGACTTCTTGATATCAGTGATGAAAGTAGTGGAGAAAGAAATGCAAGT
 GGCTGTGAGTATCAGCAGTGCCCTTCAGAGTTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGGCAATGA
 GAAAGCCGACAGTGTGGTGTCCGCTCCTGGGCGACAGGCTACCTCCTCACTGTCTTCTGCACTCTTGTTCCTGG
 TTATGCGAGAGAGTGGAGATTAATTTCTCAAACCTCGAGAAAAGTGTTCAATCAAAAAGTTAAAGGCACAGTT
 ATCACTTTTACACCTCTAGTGACTTTGCTTTTAAATGAATGGACAACATGTACAGTTTTTACTATGTGGC
 CACTGTTTAAAGAGTGCTGACTTTGTTTCTCATTCAGTTTGGGAGGAAAGGAGCTGTGCATTGAGTTGGT
 TCCTGCTCCCCAAACCATGTTAAACGTGGCTAACAGTGTAGGTACAGAACTATAGTTAGTTGTGCATTGTGA
 TTTTATCACTPATATTTGTTGTATGTTTCTCATTTGTTTGGGTTTTTTTCCAACTGTGATCT
 CGCTTGTGTTCTTACAAGCAACAGGGTCCCTTCTTGCACGTAACTATGTTTCTGAAATATTAATA
 GCTGTACAGAACAGGTTTTATTTATCATGTTATCTTATTAAGAAAAGCCCAAAAGC

FIGURE 97

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQ
GSTCCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMF
VKTYGHLVMQNSELFKDLFVELKRYVVGNVNLEEMLNDFWARLLERMFLVNSQYHFTDEY
LECVSKYTEQLKPFQDVPRKLKLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHAL
LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLDFEWNNFIDAMLMVAERLEGPFNIES
VMDPIDVKISDAIMNMQDNSVQVSQKVFQCGGPPKPLPAGRISRISSESASFARSFRPHHPPEE
RPTTAAGTSLDRLVTDVKEKLQAKKFWSSLP SNVCNDERMAAGNGNEDDCWNGKGKSRYL
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNNGNDVDFDISDESSGE
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

FIGURE 98

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT
GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATCTTCAA
GCAACTTACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTCCCTCCTCCTGTTGC
TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCAC
AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAA
AGATTGGTTCTGAGAGCCCCGAGAAGAAAATTTCATGACAGTGTCTGGGCTGCCAAAGAAGC
AGTGCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAAACAAGACACCAAAGGCACCACAGA
AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAAACAATGTGAGCTAAGAAGCTT
TGCTCTGCCTTTGTAGGAGCTCTGAGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAA
GACAGTGAGCACCTACCAGACACTCTTCTTCTCCCACTCACTCTCCCACTGTACCCACC
CCTAAATCATTCCAGTGCTCTCAAAAAGCATGTTTTCAAGATCATTTTGTGTTGTCTCTC
TCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTACCAGGCTTAGGCTT
AATTACCTGAAAGATTCCAGGAAACTGTAGCTTCCTAGCTAGTGTATTAACTTAAATGC
AATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTTAAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 99

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FIGURE 100

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCCTGGGACTGCTTGTCTTATTCCTGACCT
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
AAGCCAGACTTCCCCAAATTCCTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA
GTTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA
AACATTTCATCAAAGTGAACATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA
GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC
TCCCAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAAACAGAACTCATTTTGAACACC
CTGACTGCATTTTGTCTTTTAGAAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTG
ATGGAGAGGAAA

FIGURE 102

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCT
CAGAGCTGGTCTGCCATGGACATCCTGGTCCCCTCCTGCAGCTGCTGGTCTGCTTCTTAC
CCTGCCCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCTGTGCAAAAGCTACTTCC
CCTACCTGATGGCCCTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG
CTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGCCCTACTGGAGCTGGG
CTGCGGAACCGGAGCCAACCTTTCAGTTCTACCCACCGGGCTGCAGGCTCACCTGCCTAGACC
CAAATCCCCACTTTGAGAAGTTCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
GGTGGTCTGCACTCTGGTCTGTGCTCTGTGCAGAGCCCAAGGAAGGTCTGCAGGAGGTCC
GGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTCTGGGAGCATGTGGCAGAACCATATGGA
AGCTGGGCCTTCATGTGGCAGCAAGTTTTCGAGCCACCTGGAACACATTGGGGATGGCTG
CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTTCTCCGAAATCCAATAGG
AAGCAGAGCCCCCTCCCTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGTGTC
AAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCCTTCCCCAGCCTCCAATTAGAACA
AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTAGCAGAATGAGAGAAGACATT
CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATC
CGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC
TGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCTCCCAATGTTGTC
CCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATGCGT
CTCTAGGAACTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCTCT
CTCCCCACTACCACCTTCTTCTGAGCTGGGGGACCAGGGAGAATCAGAGATGCTGGGGAT
GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGA
AACCACG

103/330

FIGURE 103

MDILVPLLQLLVLLLTPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSQL
KGLTGASGKVALLELGC GTGANFQFYPPGCRVTC LDPNPHFEKFLTKSMAENRHLQYERFVV
APGEDMRQLADGSM DVVVCTLVLC SVQSPRKVLQEVRRVLRPGGV LFFWEHVAEPYGSWAFM
WQQVF EPTWKHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLFPVGPHIMGKAVKQSF
SSKALICSFP SLQLEQATHQPIY LPLRGT

103/330

FIGURE 104

GTGGGATTTATTTAGTGCAGATCGTTTTCTCAGTGGTGGTGAAGTTGCCTCATCGCAGG
 CAGATGTTGGGGCTTTGTCCGAACAGCTCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA
 ACTAATATTTATATGACAGAAGAAAAAGATGTCATTCCGTAAAGTAAACATCATCATCTTGG
 TCCTGGCTGTTGCTCTCTTCTTACTGTTTTCACCATAACTTCCTCAGCTTGAGCAGTTTG
 TTAAGGAATGAGGTTACAGATTGAGGAATTGTAGGGCTCAACCTATAGACTTTGTCCCAA
 TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATCTG
 AAGACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTGAGCACAACTCGCTCCAAT
 GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCCTCTCCGGTCTGGCTCAACAG
 TGATTCCTGAAAAGCATCAGATACAAAATTGTCAATTTTGACCTAACTTTTGAAGGAA
 AAGTAAAGGAGGATCCTGACCAGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTAC
 TTGCCAATTCGGTTCCTCCAGCGCAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCA
 AGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAG
 AAGATTGTGATTCAGCCTCTACTAAAGTTGTATCCGTGGAGCAGGAAACCAGTACAATTAC
 ATTGGCTATCTGACTATAAAAAGGAAAGAATTTCGTAAGCTTTCCATGAAAGCCAGCACTTG
 CTCATTTAATCCTGGAGTTTTTGTGCAAACCTGACGGAATGGAACGACAGAATATAACTA
 ACCAAGTGGAAAAATGGATGAAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCTGGCT
 GGTAGCATCACACACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCGATCC
 TATGTGGAATGTCCGCCACCTTGTTCCAGTGCTGGAACGATATTCACCTCAGTTGTAA
 AGGCTGCCAAGTTACTCCATTGGAATGGACATTGAAGCCATGGGGAAGGACTGCTTCATAT
 ACTGATGTTTGGGAAAAATGGTATATTCAGACCCAACAGGCAAATTCAACCTAATCCGAAG
 ATATACCGAGATCTCAAACATAAAGTGAACAGAAATTGAAGTGAAGCAAGCATTTCTCAG
 GAAGTCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA
 GCAAGCCATGGAAAAAGATGTGTGAGCTAGGTAAAGATGACAACTGCCTGTCTGGCAGTC
 AGCTTCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTCTTCTT
 ACTACAATGCTGAATGACTGGAAGAAGAAGTATGCTAGTTGAGTCTAGCTGGTACAGA
 TAATTCAAACTGCTGTTGGTTTTAATTTTGTAACTGTGGCTGATCTGTAAATAAACTT
 ACATTTTTT

FIGURE 105

MSFRKVNIIILVLAVALFLLVLHHNFLSLSSLLRNEVTDSGIVGPQPIDFVPNALRHAVDGR
QEEIPVVIAASEDRLGGAIAAINS IQHNTRS NVIFYIVTLNNTADHLRSWLNSDSLKSIRYK
IVNFDPKLLEGKVKEPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNT
ALKPGHAAAFSEDCDSASTKV VIRAGNQYNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA
NLTEWKRQNI TNQLEKWMKLNVEEGLYSRTL AGSITTPPLLIVFYQQHSTIDPMWNVRHLGS
SAGKRYSPQFVKA AKLLHWNGHLKPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK

105/330

FIGURE 106

TGGTTTTTGCCCCATAAAATCCCTCAGCTTGAGCAGTTTGTTAAGGAATGAGGTTACAGATT
CAGGAATTNTAGGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGGCCAT
TGCAGCTATAAACAGCATTTCAGCACAACTCGNTCCAATGTGATTTTCTACATTGTTACTC
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAATTGTC AATTTTGACCTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCCCAGCG
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTAC
TAAAGTTGTCATCCGTGGAGCAGGAAA

FIGURE 107

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGCGCTAGTGGGGCTGCGCGGCTGCCACG
GAGCTAGAGGGCAAGTGTGCTCGGCCAGCGTGCAGGGAACGCGGGCGGCCAGACAACGGGC
TGGGCTCCGGGGCCTGCGCGCGGGGCGCTGAGCTGGCAGGGCGGGTGGGGCGCGGGCTGCA
TCCGCATCTCCTCCATCGCTGCAGTAAGGGCGGCCGCGCGAGCCTTTGAGGGGAACGACT
TGTCGGAGCCCTAACAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGGAGCGTCACATCACT
TTCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATT
CCGTAAAGTAAACATCATCATCTTGGTCCTGGGCTGTTGCTCTCTTCTACTGGTTTTCAC
CATAACTTCTCAGCTTGAGGCAGTTTGTTAAGGAATGAGGTTACAGATTGAGGAATGTAG
GGCCTCAACCTATAGGACTTTGTCCCAATGCTCTCGACATGCAGTAGATGGGAGACAAGA
GGAGATTCTGTGGTCATCGCTGCATCTGAAGACAGGCTTGGGGGGCCATTGCAGCTATAA
ACAGCATTCAGCACAACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA
GCAGACCATCTCCGGTCTCGGGCTCAACAGTGATTCCCTGAAAAGCATCAGATACAAAATTG
TCAATTTTGACCTTAACTTTTGAAGGAAAAAGTAAAGAGGATCCTGACCAGGGGGAATCC
ATGAAACCTTTAACCTTTGCAAGGTCTACTTGCCAATCTGGGTTCACAGCGCAAAGAAGG
CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTGCCCTTTACAATACAGCA
CTGAAGCCAGGACATGCAGCTGCATTTTCAAGAGATTGTGATTGAGCCTCTACTAAAGTTGT
CATCCGTGGAGCAGGAACCAAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAGAA
TTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCTGGAGTTTTTGTGCAAAAC
CTGACGGAATGAAACGACAGAATATAACTAACCAACTGGAATAATGGATGAAACTCAATGT
AGAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAACACCTCCTCTGCTTATCG
TATTTTATCAACGCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTTCCAGT
GCTGGAACGATATTACCTCAGTTTGTAAAGGCTGCCAAGTTACTCCATTGGAATGGACA
TTTGAAGCCATGGGAAGGACTGCTTCATATACTGATGTTTGGGGAAAAATGGTATATTCCA
GACCCAACAGGCAAATTCAACCTAATCCGAGATATACCGAGATCTCAACATAAAGTGAA
CAGAATTTGAACTGTAAGCAAGCATTTCTCAGGAAGTCTGGAAGATAGCATGCGTGGGAAG
TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAATAAGATGTGTCAGCTAG
GTAAGATGACAACTGCCCTGTCTGGCAGTCAGCTTCCCAGACAGACTATAGACTATAAAT
ATGTCTCCATCTGCCTTACCAAGTGTCTTCTACTACAATGCTGAATGACTGGAAGAAGAA
CTGATATGGCTAGTTCAGCTAGCTGGTACAGATAATTCAAACTGCTGTGTGGTTTTAATTTT
GTAACCTGTGGCCTGATCTGTAATAAACTTACATTTTCAATAGGTAAGGAAAAAAAAAAAA
AAAAAA

FIGURE 108

CTGCAGGTAGACATCTCCACTGCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
GAAGGCCGGCCATACCAGAGTCCTGCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG
TCTGTGCTGGTCTGAGGGTGCTGCCTGTCAATGGGGGCAGCCATCTCCAGGGGGCCCTCATC
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTCTGGGTCATCCTCTGCTG
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTGAATCCAGTCCCAACTCCAGCCC
TGGCCCTGTCTGAGAAGGCCCCACCACCCAGAAGCCCAGCCATGAAGGCAGCTACCTGC
TGCAGCCCTGAAGGCCCTTGGCCTAGCCTGGAGCCCAGGACCTAAGTCCACCTCACCTAGAG
CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGGTCCAGAAGTCAAGAGTCCGCCTGCT
TGGAGCTGGACCCAGCGGCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC
TAAGGAGATGGGCCTGGGGTGGGGGCTTATGAGTTGGTGTAGAGCCAGGGCCATCTGGACT
ATGCTCCATCCCAAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTTCCCTAGGCTGAGCACC
TCTAGGCCCTCTAGGTTGGGGAAGCAAAGTGAACCCATGGCAATAATAGGAGGGTGTCCAG
GCTGGGCCCCCTCCCTGCTCTCCAGTGTTTGTGGATAATAAATGGAAGTATGGCTCTAA
AAAAAAAAAAAAAAAAAA

109/330

FIGURE 109

MGA AISQ GALIA IVCNGLVG FLLLLLWVILCWACHSRLEPTLTLSLNPVPTPALAPVLRPHH
PRSPAMKAATCCSPEGPWPSLEPRT

109/330
MGA
AISQ
GALIA
IVCNGLVG
FLLLLLWVILCWACHSRLEPTLTLSLNPVPTPALAPVLRPHH
PRSPAMKAATCCSPEGPWPSLEPRT

FIGURE 110

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCAGGCTACCA
 GTTCCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTA
 CTCCTTATTTGCATCTGTTTTGATAAATGATGTTGACACCCCTCCACCGAATTCCTAAGTGGAA
 TCATGTCGGGAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCC
 ATGATGTTTACCTTCAGATTATCACCACCCCTTCTGGTTCACATTTTCATTTTCATTGTTAT
 TTTGGGATTTGTTGTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACC
 TCAGCATAGAATTGGACACAGAAAGGGAAAATATGAAGTGCCTGCTGGGGTTTGCTATCGTA
 TCCACAGGCATCACGGCAGTGTCTGCTGCTGATTTTTTGTCTCAGAAAGAGAATAAAATT
 GACAGTTGAGCTTTTCAAATCACAAATAAAGCCATCAGCAGTGTCCCTTCTGCTGTTCC
 AGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTG
 AGCCTGGGAATGCAAGGAGCTGCCAGGTTATGGAAGGCGGCCAAGTGGAAATATAAGCCCT
 TTCGGGCATTCGGTACATGTGGTCTGCTACCATTTAATTGGCCTCATCTGGACTAGTGAATTCA
 TCCTTGCCTGCCAGCAAATGACTATAGCTGGGGCAGTGGTTACTTGTTATTTCAACAGAAGT
 AAAAATGATCCTCTGATCATCCCATCCTTTCGTCTCTCTCCATTTCTTCTTCTACCATCA
 AGGAACCGTTGTGAAAGGGTCATTTTAACTCTCTGTGGTGAGGATTCCGAGAATCATTGTCA
 TGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGTCCAGGTACCTGTTCCGA
 TGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA
 TACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAATCT
 TGTCCAAGAACTCAAGTCACTTTACATCTATTAAGTCTTGGAGACTTCATAATTTTCTA
 GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCG
 GGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGCCTACTTAGTAGCC
 ATAGTTTTTTATCTGTGTTTGAAGTGTGCTGGATGCACCTTTCTGTGTTTGTGCTGTGAT
 CTGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTT
 CGTAAAGAGGAGCAACAAATTAACAATGCAAGGACAGCAGGACAAGCACTCATTAAAGGA
 ATGAGGAGGGAACAGAATCCAGGCCATTGTGAGATAGATACCCATTTAGGTATCTGTACCT
 GGAAAACATTTCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTT
 AGTGAATTTTTTTTTTAAAGACCTAATAAACCTTATCTTCTCAAAA

FIGURE 111

MSGRDTILGLCILALALSLAMMETFRFITTLVHIFISLVILGLLFVCGVLWWLYDYDTNDL
SIELDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLFQ
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPIIVM
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAYTTTAINGTDFCTSAKDAFKIL
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAQVWAVPLLLVAFFAYLVAH
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN
EEGTELQAIVR

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGGAAGCTCTCCCTGTTTCTTCCTT
 AGAATATATGTTGATGGGATTTGTGATGAGGCAAGCTCTAAGGGAAGAAGATATTCATCTCTG
 TTGGTGGAARATTTTTTGAAGAAAGATTTGCTTCTCAACAAAGGTTGTCATCTGATAT
TATGAGGACGTGTTGTTCTCACATTAAGGCATCTGTATTTGAATGTTCCTTGTTTCTCGGG
 TGACTGGAGTACATTCAAACAAGAAGACGCAAGAAGATATAAGGCGCAAGTCACTGTG
 CCTCAGATCAACTGCGATGTCAAAGCGGAAAGATCATGCATCTGAGTTCAATGTGAAATG
 TCCAGCAGGATGCGCAAGACCCCAATACCTATTTATGCACTGACGTGTATGATCATCTACT
 CCAGTGTGTGTGGCGCTGCCGTACACAGTGGTGTGCTTGATAATTCAGGAGGAAATAATCT
 GTTCGGAAGTGTCTGGACAGTCTGGTTTACAAGGGAGTATTCCAAGCGTGTCCAATCGTT
 ATCCCTTACACAGATGGAGAGCAATCTTTATCGTCTAGGAAGTAAACCCAAAAGGGGTAA
 CTTACCCATCAGCTCTTACATACATCATCTAGAAAGTCCAGCTGCCAAGCAGTGTAGAC
 ACAAAAGCTCTCAGAGGCAACCTATTCCAGGAGCAACTGCACAGCGGTCACTCTGATGCA
 GCTTCTGGCTGTACTGTAGCTGTGGCCACCCCACTTGTGCCAAGGCCATCCCCCTCTG
 CTGTCTCTACACAGCATCCCCAGACCAATCAGTGGGCCACAGGACCGAGGATGATGAT
 CTCTGGTCCAGTCCCACTACAAGACGCAAAAACAGCCCGAGAGTGTACAGGATCCA
 AAGGCAAGATCTTTCAGGAGTGCCTTCCAGAAAGCTGTGTGAGCGGATGTACAGCTGGGAC
 TTGTTCTCAAAAAGAAATTTAGACACACAGTCTTTGGAGCGATGTCTCTGGGAGATCCAAC
 TGCAAAATTTGACTTGTCTGTTTTAATTTGATTTGGGAGACCCAGCATTTGCCAAGCGGATTCGG
 AATCCAGAAGCAGCTCTGGCTGTATTTGCCAAAGCTCTTGACATTTGGCCCTGCGGTCAC
 TGATGGGTGTGTTCGATATGAGACAACCTCTGACTCACTTTAACTCTCAAGACACAG
 AATTCCTCGAGATCTGAAGACGCCATTAGAGAAAATTACTCAGAGAGGAGGACTTTCTAATGT
 AGGTCGGGCCATCTCCTTTTGACCAAGAAGTCTCTTTTCCAAAGCAATGAAACACAGAGC
 AGGCTCCCAATGTGGTGGTGTGTGATGGAGTGTGCTGGCCCGGCAAGCTGGAGGAGCT
 TCAAGATTTGCGAGAGATGAGGATCAACATTTTCTTCATCACCATTGAAGTGTCTGTGA
 AAATGAGAAGCATGTGTGGTGGAGCGCAACTTTGCAAAACAGGGCGGTGTGCAAGAACAG
 GCTTCTACTCTGCTCCAGCTGCAGAGCTGGTTTGGCCCTCCACAAGACCGTCAAGCTCTGGT
 AAGCGGGTCTGGCACTGACCGCTGGCCCTGCAGCAAGACTGCTTTGAATCTCGCTGACAT
 TGGCTTCTGTCATCGACGGCTCCAGAGTGTGGGACGGGCACTTCCTCCAGCGTCTCCAGT
 TTGTGACCAACCTCCACCAAGAAGTTTGAGATTTCCGACAGCAACGCGCATCGGGCGGTG
 CAGTACACTCAGCAAGCGGCTGGAGTTTGGGTTGCAGAACTACAGCAGCAAGCTGACAT
 CCTCACGCCATCAAGAGGGTGGGCTACTGGAGTGGTGTGCGACAGCAGCGGGGCTGCCATCA
 ACTTCGCCCTGGAGCAGCTCTTCAAGAAGTCCAAGGCCCAAGAGGAAGTTAATGATCTCTC
 ATACCCAGCGGAGGTTCTTACGACGAGCTCCGATCCCAAGCATGGCTGCCCATCGAAGG
 AGTGATACCTTATTCGATATAGCGCTTGCTTGGGCTGCCAAGAGGAGCTAGAAGTCAATGCCA
 CTCACCCCGCAGAGACCACTCTCTTCTTGTGGACAGTTTGACAGCTCCATCAGTATGTCT
 CCCAGGATCATCAGAACATTTGTACAGAGTCAACATCAGACCTCGGAAGTGAATTCAGAG
 CAGGCAGAGCAGCAAGTGTCTGTTTTACTAATCAGCTGTGGACACCCCAAGCGCTTAA
 TGGGCGACGCACGGTGCATCAAGTCTTGGCGAGGCAATGGAGAACAATGTCTTGTATTA
 TCTTTTGCATCATGCTTTTTTCATATTCAAACCTTGGAGTTACAAAGATGATCAACAAGT
 ATAGAATGAGCCAAAAGGCTACATCATGTTGAGGGTGTCTGGAGATTTTACATTTTGACATTT
 GTTTTCAAATAAATGTTTCGAATACAGTGCAGCCCTTACGACAGCTTACGTAGAGCTTTT
 GTGAGATTTTAAAGTTGTATTCTGATTTGAATCTGTGAACCTCGACAGTGTTCATTTT
 GTGATGCAATGTAGGAATGCTGATTAATGTTTGAAGGATGAAAAATAAAAAA
 AA
 AAAG

FIGURE 113

MRTVVLTMKASVIEMLVLLVTVGVHSNKETAKKIKRPFKFTVPQINCVDKAGKIIDPEFIVKC
PAGCQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSL
SLPRWRESFIVLESKPKKGVTYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQ
LLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTSSQNRPRADPGIQ
RQDPGGAAFQKPVGADVSLGLVPKEELSTQSLEPVS LGDPNCKIDLSFLIDGSTSIGKRRFR
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNSRDLKTAIEKITQRGGLSNV
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTQLPLVKRVC DTDRLACSKTCLNSADI
GFFVIDGSSSVGTGNFRTVLQFVTNLTKEFEISDTDTRIGAVQYTYEQRLEFGFDKYSSKPD
LNAIKRVGYWSGGTSTGAAINFALEQLFKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKG
VITYAIGVAWAAQEELEVIATHPARDHSFFVDEFDNLHQYVPRIIQNICTEFNSQPRN

FIGURE 114

CAGGATGAAC TGGTTGCAGTGGCTGCTGCTGCTGCGGGGGCGCTGAGAGGACACGAGCTCTA
TGCCCTTTCCGGCTGCTCATCCCGCTCGGCCTCCTGTGCGCGCTGCTGCCTCAGCACCATGGT
 GCGCCAGGTCCCGACGGCTCCGCGCCAGATCCCGCCACTACAGTTTTTCTCTGACTCTAAT
 TGATGCATGGACACCTTGCTGATTTTGGGGAATGTCTCAGAATCCAAAGAGTGGTTGAAG
 TGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCCTCTGTGTTTGAACAAACATT
 CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGAAGTAGA
 GGTGCGATGGCCCTGTTCCGGGCTCTCCTGAGAATGGCTGAGGAGGCGGCCGAAAACCTCC
 TCCCAGCCTTTCCAGCCCCACTGGCATGCCATATGGAACAGTGAACCTTACTTCATGGCGTG
 AACCCAGGAGAGACCCCTGTACCTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC
 CACCTTGAGCAGCCTCACTGGTGACCCGGTGTTTGAAGATGTGGCCAGAGTGGCTTTGATGC
 GCCTCTGGGAGAGCCGGTCAATATCGGGCTGGTTCGCAACACATTGATGTGCTCACTGGC
 AAGTGGTGGGCCAGGACGAGGCATCGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGT
 GAAAGGAGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTTAGAGTATAACAAAG
 CCATCCGGAATACACCCGCTTCGATGACTGGTACCTGTGGGTTAGATGTACAAGGGGACT
 GTGTCCATGCCAGTCTTCCAGTCCCTGGAGGCCACTGGCCTGGTCTTCAGAGCCTCATGG
 AGCATTGACAATGCCATGAGGACCTTCCTCACTACTACACTGTATGGAAGCAGTTTGGGG
 GGCTCCCGGAATTCTACAACATTCTCAGGATAACAGCTGGAGAAGCGAGAGGGCTACCCA
 CTTGCGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCACCT
 CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAAATCAGCAAGTGGAGTGCGGAT
 TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTTCTCTG
 GCCGAGACTGTGAATACTCTACCTCCTGTTTACCCAACCAACTTCATCCACAACAATGG
 GTCCACCTTCGACGCGGTGATACCCCTATGGGGAGTGATCCTGGGGGCTGGGGGTACA
 TCTTCAACACAGAAGCTACCCCATCGACCTTGCCGCCCTGCAGTCTGCCAGAGGCTGAAG
 GAAGAGCAGTGGGAGTGGAGGACTTGATGAGGAATTCTACTCTCTCAAACGGAGCAGGTC
 GAAATTTAGAAAAACACTGTAGTTGCGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC
 TCTTCTCACCAGAAAAACATGACCAGGCAAGGGAGAGGAAGCCTGCCAAACAGAAGTCCCA
 CTCTCAGCTGCCCCAGTCAGCCCTTCACCTCCAAGTTGGCATTACTGGGACAGGTTTCTCT
 AGACTCCTCAT**TAA**CCACTGGATAATTTTTTTATTTTTATTTTTTTGAGGCTAAACTATAATA
 AATTGCTTTTGGCTATCATAAAA

FIGURE 115

MPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVE
VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLSSKAGVEVEAGWPCSGPLLRMAEEAARKL
LPAFQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALM
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK
AIRNYTRFDDWYLVWQMYKGTVSMPVFQSLEAYWPGLOSLIGDIDNAMRTFLNYYTVWKQFG
GLPEFYNIPOQGYTVEKREGYPLRPELIESAMYLYRATGDPITLLELGRDAVESIEKISKVECG
FATIKDLRDHKLDRMESFFLAETVKYLYLLFDPITNFIHNNGSTFDAVITPYGECILGAGGY
IFNTEAHPIDLAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGT
LFSPENHDQARERKPAKQKVPLSCPSQPFTSKLALLGQVFLDSS

FIGURE 116

AAAGTTACATTTTCTCTGGAAGCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
 GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCTGGGCCGGCTCTAGAACA
 ATTACAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
 GAGATGGACAGAAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTTCAAAGCTGAGTCTACCA
AATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGCTTTTTCATGTGGTTTTTCT
 ACGCATTGATTCCATGTTTGTCTACAGATGAAGTGCCATTCTGCCTGCCCTCAGAACCTC
 TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCTGGAGA
 AACAGTGTACTATTCTGTGAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
 GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTGATGTCACTGATGACATC
 ACGGCCACTGTGCCATACAACCTTCGTGTGAGGGCCACATTGGGCTCACAGACCTCAGCCTG
 GAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCGACCTGGGATGGAGA
 TCACCAAGATGGCTTCCACCTGGTTATTGAGCTGGAGACCTGGGGCCCCAGTTTGAGTTC
 CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAAATGGTGAGGAGTGG
 GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCAGA
 CATTCTGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
 GAGAGGCCATTCCCTGGTACTGGCCCTGTTTGCCTTTGTTGGCTTCATGCTGATCCTTGT
 GGTGCTGCCACTGTTCTGTCTGGAAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCGTGG
 TGGTCTCTCCAGACACCTTGAAATAACCAATTACCCAGAAAGTTAATCAGCTGCAGAAGG
 GAGGAGGTGGATGCCTGTGCCAGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGGCCTGGAT
 CTCATAGGTTTGGCGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACC
 ATGAGGGGACAAGTTGTGTTTCTGTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
 GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC
 TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGGCTGCCACTTGTGGCTGAGCAACC
 CTGGGAAAAGTGACTTCATCCCTTCGGTCTAAGTTTTCTCATCTGTAATGGGGGAATTACC
 TACACACCTGTCTAAACACACACACAGAGTCTCTCTATATATACACAGTACACATAAA
 TACACCCAGCACTTGCAAGGCTAGAGGGAAGTGGTGACACTCTACAGTCTGACTGATTAG
 TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
 GGCTTGAGAGAGCCACTTTCAGAAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
 TGTTGAGTTCACTTCAAGCCCAATGCCGGTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGT
 AGGTGACCTGGAGGAAGGTCACAGCCCACTGAAAATGGGATGTGCATGAACACGGAGGATC
 CATGAAGTACTGTAAGTGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
 GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTC
 TGTTGGTAAAGTACAGAATTACGCAATAAAAGGGCCACCTGGCCAAAAGCGGTAAAAAA
 AAAAAAAAAA

FIGURE 117

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLWSPVIAIGE
TVYYSVEYQGEYESLYTSHIWIPISSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQTS
SILKHPFNRNSTILTRPGMEITKDGFLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECEVEVQGEAIPVLALFAFVGFMILIV
VVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation sites.

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

FIGURE 118

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGAAAGAAACAATGTTCTAGG
TCAAACAGAGTCTACCAAATGCAGACTTTACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGACTATTCTGTGCAATACCAGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG
ATGTCACTGATGACATCAGGCCACTGTGCCATACAACCTTTGTGTCAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGCGAACCCTTGCGGCGCAAGGG
GTTNGCGAACCCTTGCGGCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCCAC
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

FIGURE 119

CGGACGCGTGGGCGGCCACCTCCGGAACAAGCC**ATG**TGGCGGCGACGGTGGCAGCGGCGTG
GCTGCTCCTGTGGGTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGG
TCAACATCCGGGGCAAACCTGGTGTGCTGCGTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTG
AATGTGGCCAGCGAGTGGCGCTTACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG
AGACCTGGGCCCCACCACTTTAACGTGCTCGCCTTCCCCTGCAACCAGTTGGCCAACAGG
AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCGCCGCACCTACAGTGTCTCATTCCCC
ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGCCCATCTGCCTTCAAGTACCTGGCCCA
GACTTCTGGGAAGGAGCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGGAAGG
TGGTAGGGGCTTGGGACCAACTGTGTCAGTGGAGGAGGTCAGACCCAGATCACAGCGCTC
GTGAGGAAGCTCATCCTACTGAAGCGAGAAGACTT**ATAA**CACCGCGTCTCCTCCTCCACCA
CCTCATCCCGCCACCTGTGTGGGGCTGACCAATGCAAACTCAAATGGTGCTTCAAAGGGAG
AGACCCACTGACTCTCCTTCCCTTACTCTTATGCCATTGGTCCCATCATTCTTGTGGGGGAA
AAATTCTAGTATTTTGATTATTTGAATCTTACAGCAACAAATAGGAACTCCTGGCCAATGAG
AGCTCTTGACCAAGTGAATCACCAGCCGATACGAACGTCTTGCCAACAAAAATGTGTGGCAAA
TAGAAGTATATCAAGCAATAATCTCCACCCAAGGCTTCTGTAAACTGGGACCAATGATTAC
CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC
CAAAATAGGAGGCATTCAATGAACATTTTTTGCATATAAACCAAAAAATAACTTGTTATCAAT
AAAAACTTGTCATCCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTT
GTTATTTCTCTGTATTATTTTCTTCATTACAAAAGAAATGCAAGTTCATTGTAACAATCCA
AACAAATACCTCACGATATAAAATAAAAATGAAAGTATCCTCCTCAAAA

HIGH SCHOOL SENIORS

MVAATVAAAWLLLWAAACAQQEQDFDYDKAVNIRGKLVSLSEKYGVSLSLVNVASECGFTDQ
HYRALQQLQRDLGPHHFNVLAFCPCNQFGQQEPDSNKEIESFARRTYSVSPFPMFSKIAVTGTG
AHPAFKYLAQTSKKEPTWNFWKYLVPADGKVVGAWDPTVSVEEVRPQITALVRKLLILLKREDL

FIGURE 121

CGGACGCGTGGGCGGGCGGGGACGCAGGGCAAAGCGAGCCATGGCTGTCTACGTGGGATGC
 TGCGCCCTGGGAGGCTGTGCGCCGGGAGCTCGGGGGTGTGGGGGCCCCGGGCCGCCCTCTCT
 CGGAGTTGGCAGGAAGCCAGGTTGCAGGGTGTCCGCTTCTCAGTTCCAGAGAGGTGGATCG
 CATGGTCTCCACGCCCATCGGAGGCCCTCAGCTACGTTTCAAGGGTGCACCAAAAAGCATCTTA
 ACAGCAAGACTGTGGGCCAGTGCCCTGGAGACCACAGCACAGAGGGTCCCAGAACGAGAGGCC
 TTGGTCGTCCTCCATGAAGACGTCAGGTTGACCTTTGCCCAACTCAAGGAGGAGGTGGACAA
 AGCTGCTTCTGGCCCTCCTGAGCATTTGGCCCTCTGCAAAGGTGACCGGCTGGGCATGTGGGGAC
 CTAACCTCCTATGCATGGGTGCTCATGCAAGTTGGCCACCGCCAGGCGGGCATCATTCTGGTG
 TCTGTGAACCCAGCCTACCAGGCTATGGAAGTGGAGTATGTCCTCAAGAAGGTGGGCTGCAA
 GGCCCTTGTGTTCCCCAAGCAATTCAAGACCCAGCAATACTACAACGTCCTGAAGCAGATCT
 GTCCAGAAGTGGAGAATGCCAGCCAGGGGCTTGAAGAGTCAGAGGCTCCCAGATCTGACC
 ACAGTCATCTCGGTGGATGCCCTTTGCGGGGACCCCTGCTCCTGGATGAAGTGGTGGCGGC
 TGGCAGCACACGGCAGCATCTGGACCAAGCTCCAATACAACAGCAGTTCTGTCTGCCATG
 ACCCATCAACATCCAGTTCACCTCGGGGACAACAGGCAGCCCCAAGGGGGCCACCCCTCTCC
 CACTACAACATTGTCAACAACCTCCAACATTTAGGAGAGCGCCTGAAACTGCATGAGAAGAC
 ACCAGAGCAGTTGCGGATGATCCTGCCCAACCCCTGTACCATTGCCTGGGTTCCTGGGCAG
 GCACAATGATGTGTGATGTACGGTGCCACCCCTCATCTGGCCTCTCCATCTTCAATGGC
 AAGAAGGCACTGGAGGCCATCAGCAGAGAGAGAGGCACCTTCTGTATGGTACCCCCACGAT
 GTTCGTGGACATCTGAACACAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAG
 GTGTCATTGCTGGGTCCCCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAAT
 ATGAAGGACCTGGTGGTTGCTTATGGAACCAAGAGACAGTCCCGTGACATTCCGCGCACTT
 CCCTGAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCTCTCACACGGAGG
 CCCGGATCATGAACATGGAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGC
 ATCCGAGGGTACTCGCTCATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGT
 GGATCAGGACAAGTGGTATTGGACAGGAGATGTCGCCACAATGAATGAGCAGGGCTTCTGCA
 AGATCGTGGGCGCTCTAAGGATATGATCATCCGGGTGGTGAACATCTACCCCGCAGAG
 CTCGAGGACTTCTTTCACACACACCCGAAGGTGCAGGAAGTGCAGGTGGTGGGAGTGAAGGA
 CGATCGGATGGGGGAAGAGATTGTGCTGCATTGCGCTGAAGGACGGGAGGAGACACGG
 TGGAGGAGATAAAAGCTTTCTGCAAAGGGAAGATCTCTCACTTCAAGATTCCGAAGTACATC
 GTGTTTGTCAACAACCTACCCCTCACCATTTCAGGAAAGATCCAGAAATTCAAACCTTCGAGA
 GCAGATGGAACGACATCTAAATCTGTGAATAAAGCAGCAGGCGCTGCTGGCCGGTTGGCTT
 GACTCTCTCCTGTGAGAATGCAACCTGGCTTTATGCACCTAGATGTCCTCCAGCACCCAGTTCT
 TGAGCCAGGCACATCAAAATGTCAAGGAATTGACTGAACGAATAAGAGCTCCTGGATGGGTC
 CGGAACTCGCTGGGCACAAGGTGCCAAAAGGCAGGCAGCCTGCCAGGCCCTCCCTCCTG
 TCCATCCCCACATTCCCTGTCTGTCTTGTGATTTGGCATAAAGAGCTTCTGTTTTCTTT
 GAAAAAAAAAAAAAAAAA

FIGURE 122

MAVYVGMRLRLGRLCAGSSGVLGARAALSRSWQEARLQGVRFLLSSREVD RMVSTPIGGLSYVQ
GCTKKHLNSKT VVGQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG
DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVFPKQFKTQQY
YNVLKQICPEVENAQPGALKSQRLPDLT TVISVDAPLPGTLLLD DEVVAAGSTRQHLDQLQYN
QQFLSCHDPINIQTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY
HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY
DISTMCGGVIAGSPAPPELIRAIINKINMKDLVVA YGTTENSPVTF AHFPEDTVEQKAESVG
RIMPHTEARIMMEAGTLAKLNTPGELCIRGYCVMLGYWGEPQKTEEAVDQDKWYWTGDVAT
MNEQGFCIKIVGRSKDMIIRGENIYP AELEDFHHPKVQEVVGVKDDRMGEIEICACIRL
KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
314-319, 318-323, 379-384, 380-385, 409-413

N-glycosylation Site:

amino acids 282-285

FIGURE 123

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCCCAACCCCTGTACCATGCGCTGGGTTCCGTGGCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCAGTGGAGGC
CATCAGCAGAGAGAGAGGCACCTTCCTGTATGGTACCCCCACGATGTTTCGTGGACATTCTGA
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGT
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTGCGCGCACTTCCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCCGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGAGATGTCGCCAC

FIGURE 124

GAGCAGGACGGAGCC**ATG**GACCCCGCCAGGAAAGCAGGTGCCAGGCCATGATCTGGACTGC
 AGGCTGGCTGCTGCTGCTGCTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG
 TGCAGAAAGCAGATGACGGATGCTCCCGAACAAGATGAAGACAGTGAAGTGCGCGCCGGGC
 GTGGACGTCTGCACCGAGGCCGTGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGC
 AGTGCGGGGTTGCGGTTCCGGACTCCCGGCAAGAATGACCGCGGCTGGATCTTCACGGGC
 TTCTGGCGTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTC
 ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGCATACCCGCCCCAACGGCGTGGAGTG
 CTACAGCTGTGTGGGCTGAGCCGGGAGGCGTGCCAGGGTACATCGCGCGGCTCGTGAGCT
 GCTACAACGCCAGCGATCATGTCTACAAGGGTGCTTCGACGGCAACGTACCTTGACGGCA
 GCTAATGTGACTGTGTCTTGCTGTCCGGGGCTGTGTCCAGGATGAATTCTGCACTCGGGA
 TGGAGTAACAGGCCCAGGGTTCACGCTCAGTGGCTCCTGTTGCCAGGGGTCCCGCTGTAAC
 CTGACCTCCGCAACAAGACCTACTTCTCCCTCGAATCCACCCCTTGTCCGGTGCCCCCT
 CCAGAGCCCACGACTGTGGCCTCAACCACATCTGTCAACACTTCTACCTCGGCCCCAGTGAG
 ACCCACATCCACCACCAAAACCATGCCAGCGCCAACAGTCAGACTCCGAGACAGGGAGTAG
 AACACGAGGCCCTCCGGGATGAGGAGCCAGGTTGACTGGAGGCGCCGTGGCCACCAGGAC
 CGCAGCAATTGAGGGCAGTATCCTGCAAAAGGGGGGCCCCAGCAGCCCCATAATAAGGCTG
 TGTGGCTCCACAGCTGGATTGGCAGCCCTTCTGTGGCCGTGGCTGCTGGTGTCTACTG**T**
GAGCTTCTCCACCTGGAAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT
 CATCACTTCCGTTCACCACTGGACTGGGCTGGCCAGCCCCGTTTTTTCCAACATTCCC
 CAGTATCCCCAGCTTCTGTGTGCGCTGGTTTGGCGCTTTGGGAAATAAAATACCGTTGTATAT
 ATTCTGCCAGGGGTGTTCTAGCTTTTTGAGGACAGCTCCTGTATCTTCTCATCTTGTCTC
 TCCGCTTGTCTCTTGTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTACGGGAAGGTG
 AGAGAGAGGATGCTAAGCTTCTACTCACTTTCCTAGCCAGCCTGGACTTTGGAGCGTGG
 GGTGGGTGGGACAATGGCTCCCCTACTAAGCACTGCCTCCCTACTCCCGCATCTTTGGG
 GAATCGGTTCCCCATATGTCTTCTTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCGTAC
 CCAATTGCGCCTATAGTGAGTCGTA

FIGURE 125

MDPARKAGAQAMIWTAGWLLLLLLRGGAQALECYSCVQKADDGCSPNKMKTVKCAPGVDVCT
EAVGAVETIHGQFSLAVRGCGLPGKNDRGLDLHGLLAFIQLQCCAQDRCNAKNLTSRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPPVVSCYNASDHVYKGCDFGNVTLTAANVTV
SLPVRGCVQDEFCTRDGVTGPGFTLSGSCCQGSRCNSDLRNKTYFSPRIPLVRLPPPEPTT
VASTTSVTTSTSAVRPTSTTKMPAPTSQTPRQGVHEASRDEEPRLTGGAAGHQDRSNSG
QYPAKGGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

[illegible]

127/330

FIGURE 127

MELVLVFLCSLLAPMVLASAAEKEKEMDPFPHYDYQTLRIGGLVFAVVLFSVGILLILSRCK
CSFNQKPRAPGDEEAQVENLITANATEPQKQRTVQPSGGSLWNLRLLEPLDANVDA

127/330
MELVLVFLCSLLAPMVLASAAEKEKEMDPFPHYDYQTLRIGGLVFAVVLFSVGILLILSRCK
CSFNQKPRAPGDEEAQVENLITANATEPQKQRTVQPSGGSLWNLRLLEPLDANVDA

FIGURE 128

AAACTTGACGCCATGAAAGATCCCGGTCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT
CCACTCTGCCCAGGGAGCCACCCTGGGTGGTCCTGAGGAAGAAAGCACCATTGAGAATTATG
CGTCACGACCCGAGGCCTTTAACACCCCGTTCCTGAACATCGACAAATTGCGATCTGCGTTT
AAGGCTGATGAGTTCCTGAAGTGGCACGCCCTCTTTGAGTCTATCAAAAGGAAACTTCCTTT
CCTCAACTGGGATGCCTTTCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCCAGT
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT
CTTTCCTGCCTCAGGAACTCCAATAAAACATTTTCATCCAAA

FIGURE 129

MKIPVLPVAVLLSLLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSFAKDE
FLNWHALFESI KRKL PFLNWD A FPKL KGLRSATPDAQ

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FIGURE 130

CAGTTCGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGC
CTTTGCCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTT
TTCTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC
TTTGCCGGCCACTCATGAGAGTGTTTTTGTGTAAAGTATTTTTAGAACTACTGTTGACTTCT
TCATGATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCTCA
AATTTTTGTTATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCTTTATTTTT
AGGTTCAAGGTTCAATTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTGTTTATC
TTCACATATTAATTGTAACGATTAAAAAAGAATAAGAGCAGCAGACCTCTAGGAGAATATTT
TATCCCTGGGTGCCCCTGACACATTTATGTAGTGATCCCAAAATGTGATTGTTAATTTAAA
TGTATTCTAATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTT
AAAAGTTTGAGTATATTTTTCAACTAGATATTTGTATAGAAAGACTGAATAGTGATG

131/330

FIGURE 131

MGVEIAFASVILTCLSLAAGVSQVVLLQPVPTQETGPKAMGDLSCGFAGHS

131/330

FIGURE 132

GGGGAATCTGCAGTAGGTCTGCCGGCGATGAGAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG
 GCTGCTGTTGTTCCCTCCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAAATGGA
 AAGTATTTATTGACCAAATTAACAGGTCCTTGGAGAATTACGAACCATGTTCAAGTCAAAAC
 TGCAGCTGCTACCATGGTGTATAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAG
 GAAGATGATGCGAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA
 GACTGTACCGGAAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT
 TTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA
 GGTTCCTAAATGGATGGAGCCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC
 ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGGACCTGCTGTTTGGCCAATTTAT
 CCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTGAGCAGCAGAGTG
 GCCATGGAAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG
 ATCCTCTCATTTCTTCTGTCTCGGAAAAACCCAAAACCTGTGTTGATGCAGAATACACAAAAAC
 CAGGCCTGGAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGT
 GGATCACTGCAATACAAGTATCTGTTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTA
 AACACCTCTTCTGTGTGGCTCACTTGTTCATGTTGGTGATGAGTGGCTAGAATCTTC
 TATCCACAGCTGAAGCCATGGGTTCACTATATCCAGTCAAAACAGATCTCTCCAATGTCCA
 AGAGCTGTACAAATTTGTAAGCAAATGATGATGATGCTCAAGAGATTGCTGAAAGGGGAA
 GCCAGTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTG
 AGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAAATTAT
 TCCCAAAATGTTGAAAACCTGAACCTAGTAGTCATCATAGGACCATAGTCCTCTTTGTGGCA
 ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA
 TCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGCACCCAGAGCAACTCTTGAGA
 AAGATTTAAATGTGTCTAATACACTGATATGAAGCAGTTCAACTTTTGGATGAATAAGGA
 CCAGAAATCGTGAGATGTGGATTTGAACCAACTCTACCTTTTCAATTTCTTAAGCAATC
 ACAGCTTGTGCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA
 TGTGATGATGCCCTTTGTCCCATTATTTGGAGCAGAAAATTCGTCATTTGGAAGTAGTACAA
 CTCATTGCTGGAATTGTGAAATTATTCAAGGCGTGATCTCTGTCACTTTATTTTAATGTAGG
 AAACCCATAGGGGTTTATGAAAAAATCTTGGGGATCATTCTCTGAATGGTCTAAGGAAGCGG
 TAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTGTAACCATAAACTCTGTACTCAG
 GAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATGCAATTGGATT
 TCAGGTTCCCTTTTGTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

MEWASSPLRLWLLLLFLPSAQGRQKESGSKWKVFDIQINRSLENYEPSSQNCSCYHGVE
EDLTPFRGGISRKMMAEVVRRLGLTHYQITKNRLYRENDCMFSPRCSGVEHFLEIVIGRLPD
MEMVINVRDYPQVPKMWEPAPVFSFSKSTSEYHDMYPAWTFWEGGPAVWPIYPTGLGRWDL
FREDLVRSAAQWPWKKNSTAYFRGSRTPERDPLILLSRKNPKLVD AEYTKNQAWKSMKDT
LGKPAAKDVHLVHCKKYKYLNFNRGVAASFRFKHLFLCGSLVFHVGD EWLEFFYPQLKPWVH
YIPVKTDLNSVQELLQFVKANDDVAQEIAERGSQFIRNHLQMDDITCYWENLLSEYSKFLSY
NPTRRKGVDQOII PKMLKTEL

FIGURE 134

CACCCCTCCATTTCTCGCCATGCCCCCTGCACTGCTCCTGATCCCTGCTGCCCTCGCCTCTT
TCATCCTGGCCTTTGGCACCGAGTGGAGTTCGTGCGCTTTACCTCCCTTCGGCCACTTCTT
GGAGGGATCCCGAGTCTGGTGGTCCGGATGCCCGCCAGGGATGGCTGGCTGCCCTGCAGGA
CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTGTGGGCAGC
ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCTTTCAG
AGGTCACTGTATGTGGCCTGCACTGCCCTGGCCTTGCAGCTGGTGTATGCGGTACTGGGAGCC
CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCGC
TCCTCTGCTTTGTGCTCCATGTCATCTCCTGGCTCCTCATCTTTAGCATCCTTCTCGTCTTT
GACTATGCTGAGCTCATGGGCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCGAGCC
TCTGGCCCTGAAGTCTCCCGGGCTCTCAGACTCTTCTCCACCTGCGCCACCCAGTGTGTG
TGGAGCTGCTGACAGTGTGTGGGTGGTGCCTACCTGGGCACGGACCGTCTCCTCCTTGCT
TTCTCTCTTACCCTCTACCTGGGCCTGGCTCACGGGCTTGATCAGCAAGACCTCCGCTACCT
CCGGGCCCAGCTACAAAGAAAACCTCCACCTGCTCTCTCGGCCCCAGGATGGGGAGGCAGAGT
GAGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCTCTCCCACTGAATTCTAAATCCTTAAC
ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCCAAATCCATGGACTGAAGGAGATGCCCTT
CTACTACTTGAGACTTTATTTCTCTGGGTCCAGCTCCATACCCTAAATTCTGAGTTTCAGCCA
CTGAACCTCAAAGGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC
TTCACTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC
CTGACCACTCCCCTGGCACTGTTACTTGCTCTGCGCCTCAGGGGTCCCCTTCTGCACCGCT
GGCTTCCACTCCAAGAAGGTGGACCAGGGTCTGCAAGTTCAACGGTCATAGCTGTCCCTCCA
GGCCCCAACCTTGCTCACCCTCCCGGCCCTAGTCTCTGCACCTCCTTAGGCCCTGCCTCT
GGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCCTGCTCTTAACTCGATGACTTGGGGCTC
CCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAATAAAAGTCAGCCTTTTTCTAAAAAAA

FIGURE 135

MAPALLLI PAALASFILAFGTGVEFVREFTSLRPLLGIPESGGPDARQGWLAAALQDRSILAP
LAWDLGLLLLLVFGQHSLMAAERVKAWTSRYFGVLQRSLYVACTALALQLVMRYWEPIPKGPV
LWEARAEFPWATWVPLLCFVLHVISWLLIFSILLVFDYAEIMGLKQVYYHVLGLGEPLALKSP
RALRLFSLHRHPVCVELLTVLVWVPTLGTDRLLLAFLLLTYLGLAHGLDQQDLRYLRAQLQR
KLHLLSRPQDGEAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

FIGURE 136

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA
 AGAAATTGCCAAACCATGTCTTTTTTCTGTTTTTCAGAGTAGTTCCACAACAGATCTGAGTGT
 TTTAATTAAGCATGGAATACAGAAAACAACAAAAACCTTAAGCTTTAATTTTCATCTGGAATT
 CCACAGTTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTTCCCCTGGCTGCTCTA
 TCACGTGGTGTCTCCGACTACTCACCCCGAGTGTAAGAACCTTCGGCTGCGGTGCTTCTG
 AGCTGCTGTGGATGCGCTCGGCTCTCTGGACTGTCTTCCGAGTAGGATGTCACTGAGATCC
 CTCAAATGGAGCCTCCTGCTGTGTCACTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCT
 TCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTT
 ACAGACAAGACTTTCACCTTCACACTTCGAGAGCATTCAAACGTCTCTCATCAAAATCCATTT
 CTGGTCATTCTGGTGACCTCCACCCCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC
 TTGGGGTGAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTCTTATTAGGCCAAG
 AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCTTAGAGGATGAACACCTCTTTTATGGT
 GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAACCATTATGGC
 ATTCAGGTGGGTAAGTGTGTTTTGCCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG
 TTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGAGAAGTTT
 TTCACAGGTTATCTCTAATTGATAATTATTCTATAGAGGATTTTACCAAAAAACCCATAT
 TTCTTACCAGGAGTATCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTGGGTTATATAA
 TGTCCAGAGATTTGGTGCCCAAGGATCTATGAAATGATGGGTACGTTGAAACCCCATCAAGTTT
 GAAGATGTTTTATGTGCGGATCTGTTGAATTTATTAAGTGAACATTATATTCAGAAGA
 CACAAATCTTTTCTTTCTATATAGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTG
 CAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTTGGCAGGTCATGCTAAGGAACACC
 ACATGCCATTATTAACCTTCACATTCTACAAAAAGCCTAGAAGGACAGGATACCTTGTGGAAA
 GTGTAAATAAAGTAGGTACTGTGAAAAATTATGGGAGGTGAGTGTGCTGGCTTACACTG
 AACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTATTAGTC
 AGGCCCTTCAAAGATGATATGTGGAGGAATTAAATATAAAGGAATTGGAGGTTTTTGCTAAA
 GAAATTAATAGGACCAAACAATTTGGACATGTCAATTCTGTAGACTAGAAATTTCTTAAAGGG
 TGTTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAAAACAATGTAGAGTTTTATTATTG
 AACAATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAAATATA
 TGTAGTTCTGTGTCAAAAACTTCTTCACTGAAGTTTACTGAACAAAATTTTACCTGTTTT
 TGGTCATTTATAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTTAAATTA
 CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAGGATAGTGAAT
 CATTCATTACATGCAACATTTTCCAGTTACTTAAGTATGATCAGTTTATTATTGATACATCAC
 TCCATTAATGTAAGTCATAGGTCATTATTGCATATCAGTAATCTCTGGACTTTGTTAAAT
 ATTTTACTGTGGTAATATAGAGAAGAATTAAAGCAAGAAATCTGAAGA

MASALWTVLPSRMSRLSLKWSLLLLLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYIRQD
FHFRTLREHSNCSHQNPEFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEA EK
EDKMLALSLEDEHLLYGDIIRQDFLDTYNNLTLTIMAFRWTEFCNAXVMKTDTDVFIN
TGNLVKYLNLNLHSEKFFTGYPIDNYSYRGFYQKTHISYQYEPFKVFPFYCSGLGYIMSRD
LVPRIEYEMMGHVQKIFEDYVYVIGCLNLKVNIHIPEDTNLFFLYRIHLDVQCQLRRVIAAHG
FSSKEIITFWQVQMLRNTTCHY

FIGURE 138

CCTCTGTCCACTGCTTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCTT
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA
ATAACAACGGATGGGACTCCTGGAATTCCATCTGGGATTATGGAAATGGCTTTGCTGCAACC
AGACTCTTTCAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA
AAAAACATTGCAAACATGTGTCGTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGTACTATGGATTGTGGACATTT
CCTTCTGTGGAGACACGGTGGAGAACTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAATT
TTTCTCTACTAGTTATGTTTGATTTCTTTAAGTTTCAATAAAATCATTTAGCATTGAAAAAAA

FIGURE 139

MKFTIVFAGLLGVFLAPALANYNINVNDNNNAGSGQQSVSVNNEHNVANVDNNGWDSWNS
IWDYGNNGFAATRLFQKKTICIVHKMNKEVMPSIQSLDALVKEKKLQGGKPGGPPPKGLMYSVN
PNKVDDLKFKGNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

FIGURE 140

CATTCTGAAACTAACTCGTGCAGAATTGACTTTGAAAAGCATTGCTTTTTTACAGAAGTATA
 TTAACTTTTTAGGAGTAATTTCTAGTTGGATTGTAATATGAAATAATTTAAAGGGCTTCG
 CTCATATATAGGAAAATCGCATATGTCCTAGTATTAATTCCTATTGCTTACTGATTTTTT
 TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAA
 GAATAAAGTAGATTGAGTCTCCAAATTTTATGTAAGCTTCAGAAGAAGCTGGTTTGTTACATG
 CAAGCTTATAGTTGAAATATTTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGT
 TTGTTTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT
 CAGATTCGGTTGCCAACTCGTCCCCATTGGTTTCTTCTTTTTTGGTACTACAGAAGAGGAAAT
 CCAGGAAATCTGCATAGAAAACACTTAGGCTTTATACCAGAAAAAGCCAAACTATGAATTAC
 TGGAAAAAGAAGTAGAAAAAGAAAAGTAGCCCTTACAAGAAGCCAAATTTAAAGCAAAGGGA
 TTGAATCCGGATGGAAGTCCAGCCCTTTCAACCTGGGTGGATTTTCTCCAGCCTCCAAGCC
 ATCATACCAAGAGAAGTAAAAGCTGAAGAGAAATCAACCAATCTCCAAATGGTGAAGACAG
 TCAAAAAGAAGCTGAGGATAGACACAGGCTTCCAAAAGCCTTCAATAGTGTGAAGAAA
 GACAGCAAGAGAAGTAGAAATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCAGC
 TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA
 GCTCGAGATCAAGAAGCAGGTCGCGCAGTCACAGTGAAGGCCTCGAAGACATCATAATCAT
 GGTTCCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAGTTCAAACAGACATGG
 TCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGTCACTCAGATGCAG
 CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTT
 GAGAGGTCCCATAAAAGCAAGCACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG
CTGACTTTTCTTCTCTTTGAGCCTGCATCAGTTCCTTGTTTTGGCTTATCTACAGTGTGATGT
 ATGGACTCAATCAAAAACATTAACAGCAAACCTGATTAGGATTTGATTTCTTGAAACCCCTCA
 GGTCTCTAGAACACTGAGGACAGTTTCTTTTGAAAAGAACTATGTTAATTTTTTGCACATT
 AAAATGCCCTAGCAGTATCTAATTA AAAACCATGGTCAGGTTCAATTGTACTTTATTATAGT
 TGTGTATTGTTTATTGCTATAAGAAGCTGGAGCGTGAATTCTGTA AAAATGTATCTTATTTT
 ATACAGATAAAATGCAGACACTGCTCTATTAAAGTGTTTATTGTTTAAATGATGGTGAAT
 ACTTTCCTAAAGCTGTTTGTCTGCATGTGTAAAGATTTTACAAGGAAATAAAATACAAAT
 CTTGTTTTTCTTAAAAA AAAAAAAAAAAGT

FIGURE 141

MNDSLRTNVFVRFPETIACACIYLAARALQIPLPTRPHWFLFLFGTTEEEIQEICIETLRLY
TRKKPNYELLEKEVEKRKVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEK
SPISINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSRTRSRSRSHTPRRHYN
NRRSRSGTYSSRSRSRSRSHSESPRRHNNHGSPLHKAKHTRDDLKSSNRHGHKRKKSRSRSQ
SKSRDHSDAAKKHRHERGHRDRRERSRSFERSHKSKHHGGSRSRSGHGRHR

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FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA
TTTTTTGAANNTATTTCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTTTACAGAAATATAT
TANCTTTTtagagtaatttctagtttggaattgtaatatgaaattattttaaagggttcgct
CATATATAGGAAAATCGCATATGGTCCTAGTATTAAATTNNTATTGCTTACTGATTTTTTTG
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAGA
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGCTGGTTTGTTCACATGCA
AGCTTATAGTTGAAATATTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT
GTTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACTTCA
GATTCGGTTGCCAACTNGTCCCCATTGGTTTCTTCTTTTGTGACTACAGAAGAGGAAATCC
AGGAAATNTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTACTG
GAAAAAGAAGTAGAAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTAAAAGCAAAGGGATT
GAATCCGGATGGAAGCTCCAGCCCTTCAACCCTGGGTGGATTTTCTCC

FIGURE 143

GGCACGAGGCCCTCGTGCCAAGCTTGGCACGAGGGTGCACCGCGTTCTCGCACGCGCTC**ATG**GC
 GGTCTCGGAGTACAGCTGGTGGTGACCCCTGCTCACTGCCACCCTCATGCACAGGCTGGCGC
 CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTTTGTTCGGATACAAAGCACCCG
 TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG
 GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCCGAGATGCCCCGTTCCAGCTGG
 AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTCGCGTTCTTCTCTGGAGTACCAGTGG
 TTTGTGGACTTTGTCTGTACTCGGGCGCGGTGTACCTCTTACAGAGGCCCTACTACTACAT
 GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTCTGGTGCCTGCTCACGGTGACCTTCT
 CCATCAAGATGTTCTTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGGTGAGCGC
 TCTGTCTGCCTCACCTTTGCCTTCCTCTTCTGCTGCTGGCCATGCTGGTGCAAGTGGTGCG
 GGAGGAGACCCCTCGAGCTGGGCGCTGGAGCCTGGTCTGGCCAGCATGACCCAGAAGTTAGAGC
 CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCCTGTGGCCAAGCTGGCTATCCGCGTG
 GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCTTCCTCACCTTCCAGGCCTGCGGCTGGC
 CCAGACCCACCGGGACGCACTGACCATGTGCGAGGACAGACCCATGCTGCAGTTCTCTCTGC
 ACACCAGCTTCCTGTCTCCCTGTTCATCCTGTGGCTCTGGACAAAGCCATTGCACGGGAC
 TTCTTGCAACAGCGCCGCTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCCTCGA
 CTCTGGGCGCCTCTGGTTGCTGGTGGTGTGTGCTGCTGCGGCTGGCGGTGACCCGCGCCC
 ACCTGCAGGCCTACCTGTGCTTGCCAAAGGCCCGGGTGGAGCAGCTGCGAAGGGAGGCTGGC
 CGCATCGAAGCCCGTGAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT
 GAGCTTGCAGTACCTGACGCCGCTCATCCTCACCTCAACTGCACACTTCTGCTCAAGACGC
 TGGGAGGCTATTCTTGGGGCTGGGCCAGCTCCTCTACTATCCCCGACCCATCCTCAGCC
 AGCGCTGCCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGCGGATTGCCGG
 GGCCCTGGGTGGCCTGCTTACTCCCTCTTCTCCGTGGCGTCTTGGCCTACCTCATCTGGT
 GGACGGCTGCCTGCCAGCTGCTCGCCAGCCTTTTCGGCCTCTACTTCCACCAGCACTTGGCA
 GGCTCC**TAG**CTGCCTGCAGACCCTCCTGGGGCCCTGAGGTCTGTTCTTGGGGCAGCGGGACA
 CTAGCCTGCCCCCTCTGTTTGCGCCCCCGTGTCCCCAGCTGCAAGGTGGGGCCGGACTCCCC
 GCGGTTCCCTTTCACCACAGTGCTGACCCGCGGCCCCCTTGGACGCCAGTTTCTGCTCTCA
 GAACTGTCTCTCTGGGCCAGCAGCATGAGGGTCCCAGGCCATTGTCTCCGAAGCGTATG
 TGCCAGGTTTGTAGTGGCGAGGGTGTGCTGGCTGCTCTTCTGAACAATAAAGGAGCATGCC
 GATTTTTAA

FIGURE 144

MAVLGVQLVVTLLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEELRALAGKPRPRGRKE
RWANGLSEEKPLSVPRDAPFQLETCPLTTVDALVLRFFLEYQWVFDAVYSGGVYLFTEAYY
YMLGPAKETNIAVFWCLLTVTFSIKMFLTVTRLYFSAEEGGERSVCLTFAFLFLLLAMLVQV
VREETLELGLEPGLASMTQNLEPLLKKQGDWALPVAKLAIIRVGLAVVGSVLGAFLTFPGLR
LAQTHRDALTMSEDRPMLQFLLHTSFLSPLFILWLWTKPIARDFLHQPPFGETRFSLLSDSA
FDSGRLWLLVVLCLLRLAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVRVYCYVT
VVSLOYLTPILITLNCTLLKTLGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVOQQTAAARI
AGALGGLLTPLFLRGVLAYLIWWTAACQLLASLFGLYFHQHLA

FIGURE 145

CGTTNGCACGCGTCAATGGCGGTCTCGGAGTACAGCTGGTGGTGACCCTGCTCACTGCCAC
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTT
TGTTCCGATACAAGCACCCGTNTTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC
CAGAGGCAGGAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC
GAGATGCCCCGTTCCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCCTGCGC
TTCTTCTCGGAGTACCAGTGGTTTGTGGACTTTGCTGTGTACTCGGGCGGCGGTACCTCTT
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCTGACAGTGACACGGCTGTACTTCAGC
GCCGAGGAGGGGGTGAGCGCTCTGTCTGCCTCACCTTGCCTTCCTCTTCTGCTGCTGGC
CATGCTGGTGCAGCG

FIGURE 146

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGGCCGTGATTTATTAACGTGGCTT
 AATCTGAAGGTTTCTCAGTCAAAATCTTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCTTAAAGGAGC
 TTGGCTGGTTTGGGCCCTTTAGAGCTGACAGAAGGTGGCCAGGGAGAAATGCAGCACACTGCTCGGAGAAATGAAGG
 CGCTTCTGTTGCTGGTCTTGCCCTGGCTCAGTCTCGTCTAATACATTTGCAAAATGTGGGCAACCTGCACCTTCTGT
 TATTGAGAATCTGTAAAGGTGCTCCCACTACGGCTGACCAAAAGATAGGAAGAGGCGCTCACAAGATGGCTG
 TCCAGACGGCTGTGGGAGCTCAGACCCACGGCTCCCTCCCCAGAGTTTCTGCAAGCTGCCACCATCTCTCTTAA
 TGACAGACGAGCCTGCGCTACACAACCTGGCTACGTGTCTCGGCAGAGGACGGGCGAGCCAGCAATCAGCCCA
 GTGGAATCTGGCCGGAGCAACCCAACTAGGGCAGCGCCCTTTGAGAGATCCACTATTAGAGCAGATCAATTTAA
 AAAAATAAATCAGAGCTTTGAGTGTCTTCGAAGGACAAAGAGCGGAGTGAGTTGCCAACCATGCCGACGAGG
 CGAGGGAAAAATCTGAAAACACCACTGCCCCCTGAAGTCTTTCCAAAGTTGTACCACTGATTCCAGATGGTGAA
 ATTACAGCATCAAGATCAATCGAGTAGATCCCAGTGAAGGCTCTCTATTAGGCTGGTGGGAGGTAGCGAAAC
 CCCACTGGTCCATATCATTATCCAACACATTTATCGTGATGGGGTGATCGCCAGAGACGGCCGGCTACTGCCAG
 GAGACATCATTCTAAGGTCAACGGGATGGACATCAGCAATGTCCCTCACAACTACGCTGTGGCTCTCTCTGGG
 CAGCCCTGCCAGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCCGAGCAGGAACAATGGACAGGCCCC
 GGTGCTTACAGACCCCGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGGAA
 TAAAACTGGTGGCGAAGTGGATGAGCCTGGGGTTTTCATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGA
 CATGGTCAGCTTGAGGAGATGACCGGTGTGTAGCCATCAATGGACATGATCTCGATATGGCAGCCAGAAAG
 TGCGGCTCATCTGATTACGGCCAGTGAAGACGTGTTACCTCGTGTGCCGCCAGGTTTGGCGAGCGGAGCC
 CTGACATCTTTAGGAAGCCGGCTGGAAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACACT
 CCCAAGCCCCCTCCATCTCAAAATTAATCTGTGATGAGAAGTGGTAAATATCCAAAAGACCCCGGTGAATCTCT
 CGGCATGACCGTCGAGGGGGAGCATCACATAGAGAATGGGATTTGCCTATCTATGTATCATAGTGTGAGCCCG
 GAGGAGTCATAAGCAGAGATGGAAGAATAAAAACAGGTGACATTTTGTGAATGTGGATGGGTCGAACCTGACA
 GAGGTGACCCGGAGTGAGGCAGTGGCATTATTGAAAAGAACATCATCTCGATAGTACTCAAAGCTTTGGAAGT
 CAAAGAGTATGAGCCCCAGGAAGACTGCAGCAGCCGAGCAGCCCTGGACTCCAAGCACCAATGGCCCCACCCA
 GTGACTGGTCCCCATCTGGGTGATGTGGCTGGAATTACACGGTGCTGTGTAACTGTAAAGATATTGTATTA
 CGAAGAAACACAGCTGGAAGTCTGGGCTTCTGCAATGTAGGAGGTTATGAAGAATACAATGGAAACAAACCTTT
 TTTCAATCAATCCATTTGTTGAAGAACACAGCATCAATGATGGAAGAATTAGATGTGGTGATATTTCTCTTG
 CTGTCAATGGTGAAGATACATCAGGAATGATACATGCTTGGTGGCAAGACTGCTGAAGAAGCTTAAAGGAAGA
 ATTACTCTAATATTGTTTCTTGGCTGGCACTTTTTTATGAATCAATGATGGGTGAGAGGAAACAGAAAAA
 TCACAAATAGGCTAAGAGTTGAACACTATATTTATCTTGTCAGTTTTTATATTTAAAGAAAGAAATACATTGT
 AAAAATGTCAAGAAAGATGATCATCTAATGAAGGCCAGTTACACCTCAGAAAAATATGATTTCAAAAAATTA
 AAATACTAGTTTTTTTTTCACTGTGGAGGATTTCTCATTACTCPACAACTATGTTTTATATTTTTTCTATTCAAT
 AAAAGCCCTAAACCACTAAATGATTGATTGTATACCCCACTGAATTCAGCTGATTTAAATTTAAATTTT
 GGTATGTGAAGTCTCCCAAGGATCAATTATGGCCATTTTAAATTTACAGCTAAATATTTTTTAAATGCA
 TTGCTGAGAAGCTTGCTTTTATCAACAAAGATAAATATTTTTTCAGAGTTAAA

FIGURE 147

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTAT
APSPEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSRS
FKKINRALSVLRRTKSGSAVANHADQGRENSENTTAPFVPRLYHLIPDGEITSIKINRVDP
SESLSIRLVGGSETPLVHIIIQHIYRDGVIARDGRLLPGDIILKVNMGDISNVPHNYAVRLL
RQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVKRVDEPGV
FIFNVLDGGVAYRHGQLEENDRVLAINGHDLRYGSPESAHLIQAASERRVHLVVSQRQVRS
PDI FQEAGWNSNGSWSFGPGRSNTPKPLHPTITCHEKVNIQKDPGESLGMTVAGGASHRE
WDLPIYVISVEPGGVISRDGRIKTGDILLNVGDVELTEVSRSEAVALLKRTSSSIVLKALEV
KEYEPQEDCSSPAALDSNHNMAPPSDWSPSWMMWLELPRCLYNCKDIVLRNTAGSLGFCIV
GGYEEYNGNKPFIFIKSIVEGTPAYNDGRIRC GDILLAVNGRSTSGMIHACIARLLKELKGRI
TLTIVSWPGTFL

FIGURE 148

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT
GCACAGGGCAGCTTTACTTACTCCAGCACCTTCTCTCCCAGGCAAATGTTGCTGACCATCT
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC
AATGTTTCAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC
AGGATCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGC
TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG
GGTCAAGTACAACCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTCAC
CCATTGAGAACTCTGCAACATATCCCTTTGTATAAGGGGAAGTGGTTGAAAACACACAT
AATGTCGGTGTCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTG
TGCAGACATTGATGTTTAGGATGATTAGCCCTCTGTGTTTATCTTTTCAAAGAAATACATCC
TTGGTTTCACTCAAAAGTCAAATTAATTCTTTCCCAATGCCCAACTAATTTTGAGATTC
AGTCAGAAAATATAAATGCTGTATTATA

149/330

FIGURE 149

MKILVAFLLVLTIFGIQSHGYEVFNII SP SNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTT
IFDYKHGYIASRVLSRRACFILKMDHQNI PPLNNLQWYIYEKQALDNMFSNKYTWWKYNPLE
SLIKDVDWFLLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

149/330

FIGURE 150

GGCACGAGCCAGGAAGTAGGAGGTTCTCACTGCCCCGAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCACAAAGTCCTGGAAGTTTTCCCAAAG
GCCGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACCGCCATCACCTATTCCCTC
TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGGTGGTGAAGACCCACGAGCCGGCCTCCTT
CAACCTCAACGTCACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCCT
CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
CCAGTGTCTGAGCTGCGGGCCAACTTCACTCTGCAGGACAGAGGGCAGGCCCCAGGGTGA
GATGATCTGCCAGGCGTCTCGGGCAGCCACCTATCACCAACAGCCTGATCGGAAGGATG
GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCCGCG
AGCCAGACATCGGACTGGTTCTGGTGCCAGGCTGCAAACAACGCCAATGTCCAGCACAGCGC
CCTCACAGTGGTGCCCCCAGGTGGTGACCAGAAGATGGAGGACTGGCAGGCTCCCTGGAGA
GCCCCATCCTTGCCCTTGCCGCTCTACAGGAGCACCCGCGCTGAGTGAAGAGGAGTTTGGG
GGGTTCAGGATAGGAATGGGGAGGTCAGAGGACGCAAGCAGCAGCCATG**TAG**AATGAACC
GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCACTGTTCTGATTGGGA
GTTTCATGCAAAATGAGTGTGTTTTAGCTGCTCTGCCACAAAAAAAAAAAAAAAAAAAAA

FIGURE 151

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLVFFPKGRWVLITCCAPQPPPPITYSL
CGTKNIKVAKKVVKTHEPASFNLNVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELNANFTTLQDRGAGPRVEMICQASSGSPFITNSLIGKDGQVHLQQRPFCHRQPANFSFLP
SQTSDWFWCQAANNANVQHSALTVVPPGGDQKMEDWQGPLESPILALPLYRSTRRLSEEEFG
GFRIGNGEVRGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

FIGURE 152

GGTCCTTAATGGCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG
CTGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCTCACTCTCTTTGCTATGACATCACCGT
CATCCCTAAGTTAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGA
CTTTTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCCTGGGGAAGAAA
CTAAATGTCACAACGGCCTGGAAAGCACAGAACCAGTACTGAGAGAGGTGGTGGACATACT
TACAGAGCAACTGCGTGACATTGAGTGGAGAATTACACACCAAGGAACCCCTCACCTGC
AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGT
TTCGATGGGCAGATCTTCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC
TGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATT
ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACC
CTGGAGCCAAAGTGCAGGAGCACCCTCGCCATGTCCTCAGGCACAACCCAACTCAGGGCCAC
AGCCACCACCCCTCATCCTTTGCTGCCTCCTCATCATCCTCCCTGCTTCATCCTCCCTGGCA
TCTGAGGAGAGTCCTTTAGAGTGACAGGTTAAAGCTGATACCAAAAGGCTCCTGTGAGCAGG
GTCTTGATCAAACCTCGCCCTTCTGTCTGGCCAGTGCCACGACCTACGGTGTATGTCCAGT
GGCCTCCAGCAGATCATGATGACATCATGGACCAATAGCTCATTCACTGCCTTGATTCCCTT
TTGCCAACAAATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACC
TGATGGAATTCCTGCACCTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTC
TCTTTTGTGTTGGAAAATCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAATGATATT
GTCAGTAAATAATCACGTTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCCTGAAAGAG
AATTTTAAATTATTTAATAAGAAAAAATTTATATTAATGATTGTTTCTTTAGTAATTTAT
TGTTCTGTACTGATATTTAAATAAAGAGTTCTATTTCCTCAAAAAAAAAAAAAAAAAAAAA

FIGURE 153

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCVAQGQVDEKTF
HYDCGNKTVTPVSPLGKKLNVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

FIGURE 154

GGGAAAGCCATTTGAAAACCCATCTATACAACTATATATTTTCATTTCTGCTGCTAGCTG
CCTTGGGCCTCACAATTTTCATTCTGTTTTCTGACTTTCAAGTTATATACCGTGGAAATGGAG
TTGATCCCAACCATAACATCGTGGAGGGTTTAAATTTTGGTGGTAGCCCTCACCAATTCTG
GTGTGGCTTTCTTTGCAGAGGATTCCACCTTCAAAATCATGAACTCTGGCTGTTGATCAAAA
GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAAGAAGCTAGCAGAAGAC
TCAACCTGGCCTCCCATAAACAGGACAGATTATTCAGGTGATGGCAAAAATGGATTCTACAT
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATGGGAGGCCAAC
CCACAGAACAGCATTTCTGGGCCAGGCTGTAATCAGAATTGTCGTCGTACATGCTCAACAGC
ATTGCTTTTTTCCCCAAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCCTTACCTTT
CCTCTCTCCATTCAAGCATTCAAAGTATATTTCAATGAATTAACCTTGCAGCAAGGGACC
TTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAATGCATTTCCTGTAT
CATCCTTTTCAATAAACTGTATTCATTTTGAAAAAAAAAAAAAAAAAAAAA

155/330

FIGURE 155

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHFWLLIKREFGFYSKSQYRTWQKLA
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRKLKLGQPTQHFWARL

030808Z JUL 67

GTTCCTCCTTTCGGAGCCAAAATCCCAGGCGAGGTTGAATTATGAACGTGCCACACC**ATG**AAG
CTCTTTGGTGCGAGTAACTGTGCACACACCACTGGAAATGCATCTGCTGCCGTCTGTCTA
CCTCAGCGGCCAAGTGTGGAATCTGTGTGCAGCATTGCTGTCGCCCTCAGCGGCCCTCA
AGAATCTGCCCTTCGTTTGCTGTGCAGTAACCAAGTTACAGAAAGTGGTGTGCACGCGCCG
GGCTCTCCGAGGTCCCGCAGGGTATTCCTCGAACACCGCTACCTCAACCTCATGGAGAA
CAACATCAGATGATCAGGCCGACACCTTCGCCACCTCCACCACTGGAGGTCTCGAAT
TGGGCAGGAATCCATCCGGCAGATTTAGGTGGGGGCTTCAACGGCTGGCCAGGCTCAA
CCCCTGGAAGCTGTTCGACACTGGCTGACAGTATCTCTGAGCGGGGCTTTGAATACCTGTC
CAAGCTCGGGAGCTCTGGCTTCGCAACACCCATCGAAAGATCCCTCTTAGCCTTCA
ACCGGTCGCCCTCCCTCATGCGCTGGACTTTGGGGAGCTCAGAAGCTCGAGTATATCTCT
GAGGAGCTTTTGAAGGGCTTTCAACCTCAAGTATCTGAATCTGGGATGTGCAACATTA
AGACATGCCCAATCTCACCCCCCTGGTGGGGCTGGAGAGCTGGAGATGTCAGGGAACCAT
TCCCTGAGATCAGGCCTGGCTCTCTTCATGGCTGAGCTCCCTCAAGAAGCTCTGGGTATG
AACTCAGAGGTACGCTTGATTGAGCGGAATGCTTTGACGGGTGGTCTCACTTGTGAAT
CAACTTGGCCCAATAAACCCTCTCTTCTTTGCCCATGACCTCTTTACCCCGCTGAGGTACC
TGGTGGAGTGTGATCTACACCAACCCCTTGGAACTGTGATTGTGACATCTGTGGTCTAGC
TGGTGGCTTCGAGAGTATATACCAACCAATTCACCTGCTGGTGGCCGCTGTCATGCTCCAT
GCACATGGCAGGCCGCTACCTCGTGGAGGTGGACAGGCCCTCTTCAAGTCTCTGCCCCCT
TCATCATGGAGGCACCTCGAGACCAACATTTCTGAGGCTCGGATGGCAGAACTTAAGTGT
CGAATCCCCCTATGCTCCGTGAAGTGGTTGCTGCCAAATGGGACAGCTGCACGACGC
CTCCGCCACCCAGGATCTCTGTCTCAACGACGGCACCTTGAATTTTCCACAGTGCCTG
TTTCAGACATCGGGGTGTACACATGATGTTGACCAATGTTGCAGGCAACTCCAACGCTGC
GCCTACCTCAATGTGAGCACGGCTGAGCTTAACACCTCCAACTACAGCTTCTCACCACAGT
AACAGTGGAGACACGAGGATCTGCCTGAGGACACACCGGAAAGTACAGCGCTTGCTTA
CCAGTCACTGTTTACGAGCCGGATACACACCTCTACACCGTGTCTATTACAGATACC
CGTGTGCCCAAGCAGGTGGCAGTACCCGCGACAGACACCACTGACAAGATGCAGACCAGCCT
GGATGAAGTCATGAAGACCAACAGATCATCATTTGGCTGCTTTGTGGCAGTACGCTGCTAG
CTGCCGCATGTGTATGTCTTCTATAAACTCGTAAGCGGACAGCAGCGGAGTACAGTC
ACAGCGCCGCCGATCTTGTAGATATCCAGGTGGACGAAGACATCCGAGCAACACATCCG
AGCAGCAACAGCAGCTCGTCCGCTGTATCAGGTGAGGGGGCAGTAGTGCTGCCCAATTC
ATGACCATATTAACATAACACCTTCAAAACAGCAGATGGGGCCCATGGACAGAAAACAGC
CTGGGGAACCTCTGCACCCACAGTCACCACTATCTCTGAACCTTATATAATTCAAGCCA
TACCAAGGACATGCTGTACAGAACTCAAAT**TGA**CTCCCCCTCCCCAAAACCTTATAAAAT
GCAATAGAATGCACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTTTCTTGTA
TATGCTTATATATAAGTCTATGGGCTGGTTAAAAAAAACAGATTATATAAAATTTAAAG
CAAAAAGTAAAAACA

FIGURE 157

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAAASAGPQNCPSVCSCSNQFSKVVCT
RRGLSEVPQGI PSNTRYLNL MENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY
ISEGAFEGFLFNLKYLNLGMCNIKDMPNLTPLVGLLEELEMSGNHFPPEIRPGSFHGLSSLKKLW
VMNSQVSLIERNAFDGLASLVELNLAHNNLSSLPHDLFTPLRYLVELHLHHNPWNCDILW
LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAEL
KCRTPPMSSVKWLLPNGTVLSHASRHPRI SVLNDGTLNFSHVLLSDTG VYTCMVTNVAGNSN
ASAYLNVSTAE LNTSNYSFFT TVTVETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQ
TTRVPKQVAVPATD TTDKMQTSLDEV MKTTKIIIGCFVAVTLLAAAMLIVFYKLKRHQORS
TVTAARTVEIIQVDEDIPAATSAAATAAPSGVSGEGAVVLP TIHDHIN YNTYKPAHGAHWTE
NSLGNLSLHPTVT TISEPYIIQTHTKDKVQETQI

FIGURE 158

CGCTCGGGCACCAGCGCGGGCAAGC**ATG**GAGCTGGGTGCTGGACGCA**GT**TGGGGCTCACTTTCTTCAGCTCC
TTCCTCATCTCGTCTTCCCAAGAGAGTACACAGTCATTAA**T**GAAGCCTGCCCTGGAGCAGAGTGGAAATATCATG
TGTGGGAGTCTGTGAATATGATCAGATTGAGTGCCTGCGCCCGGAAAGAGGGAAGTCTGTGGGTATACCAT
CCCTTGTCTGAGGAATGAGGAGAA**T**GAGTGTGACTCCTGCCTGATCCACCCAGGTTGTACCTCTTTGAAAAC**T**
GCAAGAGCTGCCGAATGGCTCATGGGGGGTACCTTGGATGACTCTTATGTGAAGGGGTTCTACTGTGCAGAG
TGCCGAGCAGGGCTGGTAGGAGGAGACTGCATGCGATGTGGCCAGGTTCTGCGCAGCCAAAGGGCTCAGATT**TT**
GTTGGAAGCTATCCCTAACTGCTCACTGTGAATGGACATT**CAT**GCTAAACCTGGGTTTGTCACTCAACTAA
GATT**TT**GTGATGTTGAGTCTGGAGTTT**GACT**TACATGTGCCAGTATGACTATGTTGAGGTTCTGATGGAGCAAC
CGCGATGCCAGATCATCAAGCGTCTCTGTGCAACGAGCGGCCAGCTCCTATCCAGAGCATAGGATCTC**CACT**
CCACGCTCTCTTCCACTCCGATGGCTCCAAGAA**TTT**GACGGTTTTCCATGCCATTATGAGGAGATCACAGCAT
GCTCCTCATCCCTTCTTCCATGACGGCAGCTGCTCCTTGACAGGGCTGGATCTTCAAGTGTGCTGCTTG
GCAGGCTATACTGGGCAGCGCTGTGAAAATCTCCTTGAAGAAAGAACTGCTCAGACCTGGGGGGCCAGTCA**A**
TGGGTACCAAGAAATAAAGGGGGCCCTGGGCTTATCAACGGAAGCCATGCTAAAT**TGG**CACCGCTGGTGTCTT
TCTTTTGAACACTCCTATGTTCTTAGTGGCA**T**GAGAAAGAACTTGCCAGCAGAA**T**GGAGAGTGGTCAGGG
AAACAGCCCATCTGCATAAAGCCTGCCGAGAACCAAGATT**T**CAGACCTGGTGAGAGGAGAGATTCTCCGAT
GCAGGTT**CAGT**CAAGGGAGACACCATTA**CAC**CACTATACTCAGCGGCTT**CAG**CAAGCAGAACTGCAGAGTG
CCCTTACCAAGAGCCAGCCCTTCCCTTTGGAGATCTGCCATGGGATACCAACATCTGCATACCCAGCTCCAG
TATGAGTGCATCTCACCTTCTACCGCCGCTGGGCAGCAGCAGGAGGACATGCTGAGGACTGGGAAGTGGAG
TGGGCGGGCACCATCTGCATCCCTATCTGCGGGAAAT**T**GAGAACATCACTGCTCCAAGACCCAGGGTTGC
GCTGGCCGTGGCAGGCAGCCATCTACAGGAGGAC**CAG**CGGGTGATGACGCGAGCCTACACAGGGAGCGTGG
TTCTTAGTCTGACGCGGTGCCCTGGTGAATGAGCGCACTGTGGTGGTGGCTGCCACTGTGTTACTGACCTGGG
GAAGGTACCATGATCAAGACAGCAGACCTGAAAGTTGTTTGGGAAAT**T**TACCGGGATGATGACCGGGATG
AGAAGACCATCCAGAGCCTCAGATT**TT**GTCTATCATTCTGCATCCCAACTATGACCCCATCTGCTTGTGCT
GACATCGCCATCCTGAAGCTCCTAGACAAGGCCGTATCAGCACCCGAGTCCAGCCCATCTGCTCGCTGCCAG
TCGGGATCTCAGCACTCCTTCCAGGAGTCCACATCACTGTGGCTGGCTGGAA**T**GTCTGGCAGCGTGAGGA
GCCCTGGCTTCAAGAACGACACTGCGCTCTGGGGTGGTCA**GT**GTGGTGGACTCG**T**GCTGTGTGAGGAGCAG
CATGAGGACCATGGCATCCCA**GT**GAGTGTCACTGATAACATGTTCTGTGCCAGCTGGGAACCCATGCCCTTC
TGATATCTGCACTGCAGAGACAGGAGGCATCGCGCTGTGCTCCTCCCGGGACGAGCATCTCCTGAGCCACGCT
GGCATCTGATGGGACTGGTCA**GT**GGAGCTATGATAAAACATGCAGCCACAGGCTCTCCACTGCCTTACCAAG
GTGCTGCCTTTAAAGACTGGATTGAAAGAAATATGAA**TGA**ACCATGCTCATGCACTCCTTGAGAGTGT**TT**
TGTATATCCGCTGTACGTGTGTCATTGCGTGAAGCAGTGTGGGCTGAAGTGTGATTGGCTGTGAAC**T**GG
CTGTGCCAGGGCTTCTGACTT**CAG**GGACAA**AACT**CA**GT**GAAGGTGAGTAGACCTCCATTTGCTGGTAGGCTGAT
GCCGCGTCCACTACTAGGACGCCAAT**T**GGAAGTGCAGGGCTTGAAGAGTGA**TT**CTTCCAAGAGAC**CT**
ATATACAA**AACT**CTCCCACTCCACTGACCTGCTGGTGTCTCCCAACTTTCAGTATACGAATGCCATCAGCTTG
ACCAGGGAAGATCTGGGCTTCATGGGCGCCCTTTGAGGCTCTCAAGTCTAGAGAGCTGCCTGTGGGACAGCC
CAGGGCAGCAGAGCTGGGATGGTGCATGCCTTTGTGTACATGGCCACAGTCACTGGTCTTCTTCCCTCC
CCATCTCTTGTACACATTTTAA**T**AAAT**TA**AGGGTGGCTTCTGA**ACT**ACAA**AAAAAAAAAAAAAAAAAAAA**
AA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 159

MELGCWTLQLGLTFLQLLLISSLPREYTVINEACPGAAWNIMCRECEYDQIECVCPGKREV
 GYTIPCCRNEENECDSCLIHGCTIFENCKSCRNGSWGGLTDDFYVKGFYCAECRAGWYGGD
 CMRCGQVLRAPKGQILLESYPLNAHCWTIHAKPGFVIQLRFVMSLEFDYMCQDYDEVVRD
 GDNRDGQIIKRVCGNERPAPIQSIGSSLHLVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDG
 TCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV
 VSFFCNNSYVLSGNEKRTCQONGESGKQPICIKACREPKISDLVRRRVLPMPQVQSRETPH
 QLYSAAFSKQKLQSAPTKKPALPFGDLPMPGYQLHHTQLQYECISPFYRRLGSSRRTCLRTGK
 WSGRAPSCIPICGKIENITAPKTQGLRWPMQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNE
 RTVVAHAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLD
 ADIAILLDKLARISTRVQPICLAASRDLDSTFSQESHITVAGWNVLADVRSPFGKNDTLRS
 VSVSVKLLDCEEHGHVQIPSVSTNDMFCASFEPTASDICTAETGGIAAVSFPGRASPEPR
 WHLMGLVSWSYDEKTCSHRLSTAFTKVLFPKFDWTERNMK

FIGURE 160

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAGAGCTCAACTTGA
AGCTTTCTTGCTGCAGTGAAGCAGAGAGATAGATATTATTCACGTAATAAAAAACATGGCG
TTCAACCTGACTTTCCACCTTTCTACAAATTCGATTACTGTGTGTTGACTTTGTGCCT
GACAGTGGTTGGTGGGCCACCAGTAACTACTTCGTGGTGCCATTCAAGAGATTCTTAAAG
CAAAGGAGTTTATGGCTAATTTCCATAAGACCCTCATTTTGGGGAAGGGAAAAACTCTGACT
AATGAAGCATCCACGAAGAAGGTAGAACTTGACAACCTGTCCTTCTGTGTCTCCTTACCTCAG
AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAAATC
CCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTCGCCATC
CTCGTTCCCCACCGAACAGAGAGAAACCTGATGTACCTGCTGGAACATCTGCATCCCTT
CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCACTCCACCAGGCTGAAGGTAAAAAGT
TTAATCGAGCCAAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGGAC
TGCTTTATATTCACAGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGA
GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG
GATATTTTGGGGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCT
AACAACACTGGGGATGGGGAGGCCAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAG
AATGAAAAATTTCCGGCCCCCTGCCTGAAGTGGGTAAATATACAATGGTCTTCCACACATAGAG
ACAAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACCCAAGTGTACGAGTCTGG
AGAACAGATGGGTTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATA
TATCAACATCACAGTGGAATTTCTGGTTTGGTGCATGACCCTGGATCTTTTGGTGATGTTTGG
AAGAACTGATTCTTTGTTTGCAATAATTTTGGCCTAGAGACTTCAAATAGTACACACATTA
AGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTTCTTTTTGTATTTTCTTAGCAGAGCT
CCTGGTGATGTAGAGTATAAACACAGTTGTAACAAGACAGCTTTCTTAGTCATTTTGATCATG
AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAGGATGACTCAAAGGAT
AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATAT
TATGGGATAAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTCTCT
CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATTCTATTTATCTGTACAATCATCT
GTGAAGTGGTGGTGTCAGGTGAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCA
GGACACAGTGAACCTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGCGCTGCAAAGGCAG
CAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCT
TCCAGTGATGCCACCAGAGAAATACATTCTCTATTAGTTTTTAAAGAGTTTTTGTAAATGA
TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAATAATAATAAATA
TGTCATCAATACCTCTGTAGTAAATGTGAAAAAGCAAAA

FIGURE 161

MGFNLT FHLSYKFRLLLLLTCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLLLGKGT
LTNEASTKKVELDNCPSVSPYLRCQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRV
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEEN
WDCFIHFDVDLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGVTALESREQFFKVNG
FSNNYWGWGGEDDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSR
VWRTDGLSSCSYKLVSVVEHNPLYINITVDFWFGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

CTGTGGCGCGGGTGC GCAGCGGGCTGTGGCGCGCCCGAGGAGCGACCGCCGAGTTCTC
GAGCTCCAGCTGCATTCCTCCGCGCTCCGCGCCAGCTTCTCCCGCTCCGGGCGCCGCAATG
GCCAGGAGCTGTGTGCGCGCTCGCGCGATCTCTTGCTTGCTGCTCTCTGCTCCGCTGGCG
CCCGCGAGGGGTGGCCCGAGGCTGTATAGACTCAATCTCACCACCGATAGCCCTGCCACCA
CGGGAGCGGTGGTGCACCATCTCGGCCAGCCTGTGGCCGAAGGACAACCGAGCCGCTGGCCCTG
CCCGCTGACGCCACCTTACCGTTTCCATGGATCCACACCCCGTGGTGCTTACTGGCAA
GATGGAAGGGGTCTCAGCTCACCATTCCGTGTGTGTCCGCCAGCTGCCCGGGGAATTCCCGG
TCTGTGTCTGGGTCACTGCGCTGACTGTGGATGTGCCACCTGTGGCCAGGGGCTTTGTG
GTCTCTCCCATCACAGAGTTCTCTGTGGGGGACCTTGTGTGCTACCAGAACACTTCCCTACC
TGTGGCCAGCTCTATCTCACTAAGCCGCTGTGAAGTCTCTCTCTCTCTCCACAGCCGA
GCAACTTCTCAAGACCGCCTGTGTTTCTACAGCTGGGACTTCCGGGACGGGACCCAGATG
GTGACTGAAGACTCCGTGTCTTATAAATATTCCACTATCCGGAGCTTCACCGTGAAGCT
CAAGTGGTGGCGGAGTGGGAAGAGGTGGAGCCGATGCCACGAGGGCTGTGAAGCAGAAGA
CCGGGGACTTCTCCGCTCGTGAAGCTCGAGGAACCTTCGAGGATCCAAGTGTGGGG
CCCACTCTAATTCAGACTTCCAAGAAGATCACGGTGACCTTGAATCTCTCGGGGAGCCCTCC
TGTAGTGTGTGCTGGCGTCTCAAGCTGAGTGCTCCCTCCGCTGGAGGAAGGGGATGTCCACC
CTGTGTCCGTGGCCAGCAGCGTACAACCTGACCCACACCTTCAGGGACCTTGGGGACTAC
TGCTTCAGCATCCGGGCGGAGATATCATCGCAGAGACATCAGTACCAAGATCCAGGT
GTGGCCCTCCAGATCCAGCCGCTGTCTTGTCTTCCATGTGTCTACACTTACTAGCTGA
TGTGGCCTTTCATCATGTACATGACCCCTCGGAATGCCATCAGCAAAAGGACATTTGTGGAG
AACCCGAGGCCACCTCTGGGTCAAGTGCTGCTGCCAGATGTGCTGTGGGACTTTCTTGCT
SGAGACTCCATCTGAGTACCTGGAATTTGTTCTGTGAGAACCCGGGCTGCTCCGCGCCCTCT
ATAAGTGTGTCAAAATTCACCGCTCGAGGACTCCCTCCCAACCCCTCTCAGTGTATA
CTAGTCTGTGACTTGGAGTTTCCAGAGGCTGGTGTGACCACTGACACGAGGGGGTCAAT
TGCCTGGGGCTGTTGGCTGATCATTCATCTCATCTGTACAGTTTACGCCACTGCCACAAGCC
CTCCTCTCTGTTCACCCCTGACCCAGCCATTCACCATCTGTACAGTCCAGCCACTGACA
TAAGCCCCACTCGGTTACCAACCCCTTGACCCCTACCTTTGAAGAGGCTTCGTGCGAGACT
TTGATGCTTGGGGTGTTCGCTGTGACTCTCATAGTGGGCTGGCTGCCACTGCCCATTCCT
CTCATATTGGCACATCTGCTGTCCATTGGGGGTTCTCAGTTTCTCCCTCCACAGACCCCTA
CTGTGCCAGAGAGCTAGAAGAAGGTCTAAGGGTTAAAAATCCATAACTAAGGTTGTAC
ACATAGATGGGCACATCAGCAGAGAGAAGTGTGATCTGTACACACACACACACACACA
CACACACACAGAAATATAAACAGATCGCTCATATGGGCAATTCAGATGATCAGCTCTGTA
TCTGGTTAAGTCGGTTCTGGGATGACCCCTGCATCAGAGCTGAAGAGGAATTTGACCTCCA
AGGAGCCTGACAGGTTCTGGGCGCCGGGCGCTCCCTTTGTGCTTTGTCTGTGAGTTCTTGC
GCCCTTTATAAGGCCATCCTAGTCCCTGCTGGCTGGCAGGGGCTGGATGGGGGACGACT
AATACTGAGTGTGTCAGAGTGCTTTATAAATATCACTTTATTTATCGAAACCCATCTGTG
AAACTTTCTCATTAGGAAAGAGCCCTTGACAGCGGTAGAAGAGTTGAGTCAGGCGGGGCGG
TGGCTCAGCCCTGTAATCCAGACTTCTTGGGAGGCCGAGGCGGGTGGATCAGGATCAGGA
GATCAGACACACCTGGCTAAGACACCGGTGAACCCCGCTCTCTACTGAAATAACAAAAGTT
AGCCGGGCGTGGTGGTGGGTGCTGTAGTCCAGTACTCGGAGGCTGAGGACGAGGAATG
GTGCGAACCCGGGAGGCGGAGCTTGACAGTGAGCCACAGATGGCGCCACTGCACTCCAGCTGA
GTGACAGAGCGAGACTGTGCTCCA

MAQAVWSRLGRILWLACLLPWPAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHPVEFPVSVVWTAADCWMCQPVARGF
VVLPITEFLVGLDVVTTQNTSLPWPSSYLTKTVLKVSFLLHDPNSFLKTALFLYSWDFGDGTQ
MVTDSVQVYYNYSIIIGTFTVKLKVVAEWEVEEPDATRAVKQKTGDFSASLKLQETLRGIQVL
GPTLTIQVQKMTVTNLFLGSPPLTVCWRLKPECLPEEGECHPVSVASTAYNLTHTRDPGD
YCFISRAENIISCKTHQYKGIQVWPSRIQPAVFAFCCATLITVMAFIMYMTLRNATQQKDMV
ENPEPPSGVRCCCKGPFLETSPEYLEIVRENGHLLPPLYKSVKTYTV

Signal peptide:

amino acids 1-24

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

FIGURE 164

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACGATGGCACTGAGCTCCCAGATCT
GGGCCGCTTGCCCTCCTGCTCCTCCTCCTCGCCAGCCTGACCACTGGCTCTGTTTTCCCA
CAACAGACGGGACAACTTGCAAGAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTG
GATGCCCATGTTCAGAGGCGAAGGAGGCGAGACCCACTTCCCATCTGCATTTTCTGCT
GCGGCTGCTGTCATCGATCAAAGTGTGGGATGTGCTGCAAGACGTAGAACCTACCTGCCCTG
CCCCCGTCCCCTCCCTTCCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGGAATAAAA
TGGCTGGTTCTTTTGTTCACAAA
AAA

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACGATGGCACTGAGCTCCCAGATCT



FIGURE 165

DEPARTMENT OF THE ARMY

1

FIGURE 166

CTGTCAGGAAGGACCATCTGAAGGCTGCAATTGTCTTAGGGAGGCAAGTGCTGGCCCTGGC
 CTGGATCTTCCACCATGTTCTCTGTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGC
 ATCTCCCTGACTGTCTCTTCAACCTCCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTGG
 AGTCTCCTTTGGTATCCGCAAACTCTACATGAAAAGTCTGTTAAAAATCTTTGCGTGGGCTA
 CCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACCACCAGCTTTACAAGCCCTACACCAAC
 GGAATCATTTGCAAAAGGATCCCACTTCACTAGAAGAAGAGATCAAAGAGATTCTGTCGAAGTGG
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGCC
 GGAAGGAATGGAGACCATTATGGATGATGAGGTGACAAGAGATTCTCAGCAGAAGAACTG
 GAGTCTTGGAACTGCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCGGCTCAC
 GGTCTGTGGGGTTAGGAGTGCTGATTCCGTACTGCTTCTGCTGCCGCTCAGGATAGCAC
 TGGCTTTTACAGGGGATTAGCCTTCTGGTGGTGGGCACTGTGGTGGGATACTTGCCAAAT
 GGGAGGTTAAGGAATTCATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTGCGTGGC
 AGCGCTGACAGCCATCATCACCTACCATGACAGGGAAAAACAGACCAAGAAATGGTGGCATCT
 GTGTGGCCAATCATACCTCACCAGTCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCC
 ATGGTGGGTCAAGTGCACGGGGGACTCATGGGTGTGATTACAGAGAGCCATGGTGAAGCGCTG
 CCCACAGTCTGGTTTGAGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA
 CTGAACATGTGCAAGATAAAAGCAAGCTGCCTATCCTCATCTTCCAGAAGGAACCTGCATC
 AATAATACATCGTGATGATGTTCAAAAAGGGAAGTTTGAATTTGGAGCCACAGTTTATCCC
 TGTGTCTATCAAGTATGACCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAAAATACGGGA
 TGGTGACGTACCTGCTGCGAATGATGACCAGCTGGGCCATTGTCTGACGCTGTGGTACCTG
 CCTCCCATGACTAGAGAGGCGAGATGAAGATGCTGTCCAGTTTGCGAATAGGGTGAATCTGC
 CATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCTGAAGAGGGGAGAAGG
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAAACAC
 AAGGACAGGAGCCGCTCTCTGAGCGCTGCCTCCAGCTGGCTGGGGCCACCCTGCGGGGTGCCAA
 CGGGCTCAGAGCTGGAGTTGCCCGCGCCGCCCCCACTGCTGTGTCTTTCCAGACTCCAGGG
 CTCCCCGGGCTGCTCTGGATCCCAGGACTCCGGCTTTTCGCCAGCGCAGCGGGATCCCTGT
 GCACCCGGCGCAGCCTACCCCTTGGTGGTCTAAACGGATGCTGCTGGGTGTTGCGACCCAGGA
 CGAGATGCCTGTTTCTTTTACAATAAGTCGTTGGAGGAATGCCATTAAAGTGAACCTCCCA
 CCTTTGCACGCTGTGCGGGCTGAGTGGTTGGGAGATGTGGCCATGGCTTGTGCTAGAGAT
 GGCCTGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGGCGGCCACCCG
 CTCTCCAGGAAGGACAGCTGAGGCACTGTGGCTGGCTTCGGCTCAACATCGCCCCCAGC
 CTTGGAGCTCTGCAGACATGATAGGAAGGAAACTGTCTGTCGAGGGGCTTTCAGCAAAATG
 AAGGGTTAGATTTTATGCTGCTGCTGATGGGGTACTAAAGGAGGGGAAGAGGCCAGGTG
 GGCCTGTGACTGGGCCATGGGAGAACGTGTGTTTCGTACTCCAGGCTAACCCCTGAACCTCCC
 ATGTGATGCGCGCTTGTGTTGAATGTGTCTCGGTTTCCCCATCTGTAATATGAGTCGGGGG
 GAATGGTGGTATTCCTCACTCACGGGCTGTTGTGGGGATTAAAGTGTGCTGCGGGTGTGAGTA
 AGGACACATCAGTTTCACTGTTTCAAGTACAGGCCACAAAACGGGGCACGGCAGGCGCTGAG
 CTCAGAGCTGCTGCACTGGGCTTGGATTGTTCTTGTGAGTAAATAAACTGGCTGGTGAA
 TGA

FIGURE 167

MFLLLPFD SLIVNLLGISLTVLFTLLLVFIIVPAIFGV SFGIRKLYMKSLLKIFAWATLRME
RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIRRS GSSKALDNTPEFELSDIFYFCRKGME
TIMDDEVTKRFSAEELSWNLLSRTNYNFQYISLR LTVLWGLGV LIRYCFLPLRIALAFTG
ISLLVVGTTVVGYLPNGRFKEFMSKHVHLMCYRICVRALTAITYHDRENRPNGGICVANH
TSPIDV IILASDGY YAMVGQVHGGLMGVIQ RAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ
DKSKLPILIFPEGTCINNTSVM MFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMV TYL
LRMMTSWAIVCSVWYLP PMTREADED AVQFANRVKSAIARQGG LVDLLWDGGLKREKV KDTF
KEEQQKLYSKMIVGNHKDRSRS

167-2846-1

GCCCTCGAAACCAGGACTCCAGACCTCTGGTCCCGCCTCACCCGGACCCCTGGCCCTCA
 CGTCTCCTCCAGGGATGCGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCAC
 ACCTGGCAGGCCAGGCTGTTCCACCATCTGCCCTGGGCTGGCTCCAGACACCTTTGA
 CGATACCTATGTGGTGTGTCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG
 AAATGGCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCAGGAGACCTGGGAGGAC
 AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCAGAATGGAATAGCCATTATGGT
 CTACACCAACTCATCGAACACCTTGTA CTGGGAGTTGAATCAGGCCGTGCGGACGGCGGAG
 GCTCCCGGAGCTCTACATGAGGCACCTTCCCTTCAAGGCCCTGCATTTCTACCTGATCCGG
 GCCCTGCACTGCTGCGAGGCAGTGGGGGCTGCAGCAGGGGACCTGGGGAGGTGCTGTTCCG
 AGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT
 TTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCCACAGATTGGGGAGAAGAGCGGGGCTGT
 GTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCCTCCTCTCTGCCCCCTG
 GAAGACTCTGCTCTTGGCCCCCTGGAGAGTTCAGCTCTCAGGGGTGGGGCCCTGAAGTCCA
 ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG
 CAGCCTTGAGAAAGCAAGACATGGTTCGGACCACGACCTTAGCAGCCTTCTCCCAACAGG
 ATGTTGGCTGGGGAGGCACAGCAGGGCTGGGAATCTGCTATGTGATGGGACTTCTCT
 GGGACAAGCAAGGAAAGTACTGAGCAGGCACCTTGAATGAACGGTGTGCAATGTGGAGACA
 TGGAGTTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA

FIGURE 169

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGC AEEMEEKAAPLLKEEMAHH
ALLRESWEAAQETWEDKRRGLTLP PGFKAQNGIAIMVYTNSNTLYWELNQAVRTGGGSREL
YMRHFPPKALHFYLIRALQLLRGSGGCSRGPGEVVFRGVGSLRFEPKRLGDSVRLGQFASS
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPPWKTL L LAPGEFQLSGVGP



FIGURE 170

GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCA
CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG
GTCGGTTCCGTTGGTGGGGCCGTGACTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTC
TATTGTCTGGACCTTCAACACAACCCCTCTTGTACCATACAGCCAGAAGGGGGCACTATCA
TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCAGATGGAGGCTACTCCCTGAAG
CTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT
CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG
TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG
GAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTC
CCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT
GCGTTGCCAGGAACCTGTGAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGT
GAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCTCCTGTGTCTCCTGTTGTTGCCCCCT
CCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAG
AGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGCGGAAACTCCTAACATATGCCCCCAT
TCTGGAGAGAACACAGAGTACGACACAATCCCTCACATAATAGAACAATCCTAAAGGAAGA
TCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAAAGATGGAATATCCCCACTCAC
TGCTCAGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTATCTAGACAGCAGTG
CACTCCCCTAAGTCTCTGCTCA

FIGURE 171

MAGSPTCLTLIYILWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT
IQPEGGTIIIVTQNRNRERVDFFDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHV
YEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRW
GESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLCLLLVPLLLSLFVLGLFLW
FLKRERQEEYIEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPANTVYSTVEIP
KKMENPHSLLTMPDTPRLFAYENVI

FIGURE 172

CTGGTTCCCCAACATGCCTCACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC
TCTGGACCCGTAAAAGAGCTGGTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTC
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTGTCAACCATAC
AGCCAGAAGGGGGCCTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA
GATGGAGGCTACTCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGT
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
ACCAATCTGACATGCTGCATGGAACATGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT
GGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCTCTCTCTGGAGATGGGGAG
AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCGTGCAGCAGAACTTCTCAAGCCCC
ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCTCTCT
GTGTCTCTGTGGTGCCCTCTCTGCTCAGTCTCTTTGTACTGGGGCTATTCTTTGGTTTC
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCTGGGAA
ACTCCTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA
TAGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAA
AGATGGAAAATCCCCACTCACTGCTCACGATGCCAGACACCAAGGCTATTTGCCTATGAG
AATGTTATCTAGACAGCAGTGCACTCCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAAAAA

FIGURE 173

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCT
GCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCACGGGAAGGA
ACTTTAATGTAGAAAAGATTAAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTCTGGAGCAATCCATGTCTTGGAGAA
TTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGTTG
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTACT
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAAACGAAAAGGATGGGGA
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTGAGTTCAGACATCAAGGAAA
GGTTTGCACACTATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT
GCCAATCGCTGCCTCCAGGCCCGAGAATGAAGAATGGCCTGAGCCTCCAGTGTTGAGTGGAC
ACTTCTCACCAGACTCCACCATCATCCCTTCCTATCCATACAGCATCCCAGTATAAATTC
TGTGATCTGCATTCCATCTGTCTCACTGAGAAGTCCAATTCCAGTCTATCAACATGTTACC
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACACCCTTGACAAT
TTTTTCATGAAATTATTCCTCTCTCTGTTCAATAAATGATTACCCTTGCACTTAA

174/330

FIGURE 174

MKMLLLLCGLTLCVHAEESSTGRNFNVEKINGEWHITIILASDKREKIEEHGNFRLEFLEQ
IHVLENSLVLVKHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI
NEKDGETFQLMGLYGREPDLSSDIKERFAQLCEEHGILRENIIDLSNANRCLQARE

174/330
MKMLLLLCGLTLCVHAEESSTGRNFNVEKINGEWHITIILASDKREKIEEHGNFRLEFLEQ
IHVLENSLVLVKHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI
NEKDGETFQLMGLYGREPDLSSDIKERFAQLCEEHGILRENIIDLSNANRCLQARE

FIGURE 175

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA
TGGATTACGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG
TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTC
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTCAGTGTGATCA
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTC
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA
CATTATCCAGAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTCACCTCCTACTG
GTTTCAATAAACCCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC
TTCGATTCTGAAGAAAACAACATAGGCTTATCCACTTCTCAGTATTTTAGGTCTATTGCT
TGTGGAATTCTGGAGGTCTGTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGGCTGTC
TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAATGGGAATAAAATGTAAGTA
TCAGTAGTTTGAAAAAAAAA

176/330

FIGURE 176

MTCCGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA
IPATMSLTARKRACNNRTGMFLSSFFSVITVIGALYCMLISTQALLKGPLMCNSPSNSNA
NCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDEENKHRL
IHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

176/330-176/330

FIGURE 177

GTGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCT
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGCTCT
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGAGCCAAGTTGGAAGTGAAGCACTG
CACCGATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCCTGGTGAAATAGTGAA
AAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTTCAACGACACC
CTGATCTTCACTAAAAATTGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCTGC

178/330

FIGURE 178

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLEFLSDAAVNLQVAKLNPPPEALAAKLEV
KHCTDQISFKKRLSLKKSWWK

178/330

FIGURE 179

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGGCTGCAGACCCCGCCCCAGTGCCCTCTCCCCCTGCAGCCCTGCCCCCTC
GAACTGTGACCATGGAGAGAGTGACCCCTGGCCCTTCTCCTACTGGCAGGCCCTGACTGCCTTGG
AAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCAC
TCATCACTCCAGGCTCTGCCACTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGA
AGCCTAACACTGGCCCCCAGCACCTCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGCTTCTTTATGAATTAAACTCG
CCCCACCACCCCTCA

180/330

FIGURE 180

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAAGIAAVLSGKCK
YKSSQKQHSPVPEKAIPILITPGSATTC

2005-11-23 09:00

GAGGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGG**ATGT**CGCTGCTGAGCCTGCC
 TGGCTGGGCCTCAGACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTC
 CTGGCTACTCGCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAACTGCCGCGGGCTCC
 AGTGTTTCCACAGCCCCAAAACGGAACTGGTTTTGGGGTCACCTGGGCCTGATCACTCCT
 ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTGCGCCACCTATTCCAGGGCTTTACGG
 ATGGCTGGGTCCCATCATCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCA
 CCAATGCCTCAGCTGCCATTGACCCAAAGGATAATCTCTTCATCAGGTTCTCTGAAGCCCTGG
 CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGAGCGCCACCCTCGGATGCTGAC
 GCCGCGCTTCCATTTCACATCCTGAAGTCTATATAACGATCTTCAACAAGAGTGCAAAACA
 TCATGCTTGACAAGTGGCAGCAGCTGGCCTCAGAGGGCAGCAGTCTGCTGGACATGTTTGAG
 CACATCAGAGCTCATGACCTTGGACAGCTACAGAAATGCATCTTCAGCTTTGACAGCCATTG
 TCAGGAGAGGCCAGTGAATATATTGCCACCATCTTGAGACTCAGTGGCCCTTGTAGAGAAA
 GAAGCCAGCATATCCTCCAGCACATGGACTTTCGTATTTACTCTCCCATGACGGGCGCGC
 TTCCACAGGGCCTGCCGCTGGTGCATGACTTACAGACGCTGTCTCCGGGAGCGGCGTCTG
 CACCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAAAGCCAAGTCCAAGACTTTGG
 ATTTCAATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTCAGATGAGGAT
 ATAAGAGCAGAGGCTGACACCTTCATGTTTGAGGGCCATGACACCACGGCCAGTGGCCTCTC
 CTGGGTCTCTGTACAACCTTGCAGGGACCCAGAATACCAGGAGCGTGCCGACAGGAGGTGC
 AAGAGCTTCTGAAGGACCGCGATCCTAAAGAGATTGAATGGGACGACCTGGCCAGCTGCCC
 TTCCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATCTCCCG
 ATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCTCCCCAAAGGCATTACCTGCC
 TCTCGCATATTATAGGGGTCCATCACAACCCAACTGTGTGGCCGGATCCTGAGGCTTACGAC
 CCCTTCGCTTTGACCCAGACATGACATCGGAGGCTTGCCTACGGCGAGATGAGAGTGGTCTCTGG
 CGCAGGGGCCGAGAACTCATCGGCAGGCGTTCGCCATGGCGGAGTGAAGCCCGAAGAGCTGGAA
 CGTTGATGCTGCTGCACTTCCGGTTCTCGCAGACACACTGAGAGCCCGAGAGGCTTGCA
 TTGATCATGCGCGCCGAGGCGGGCTTTGGCTGCGGGTGAGGCCCTGAAATGTAGGCTTGCA
GTGACTTTCTGACCCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAAACGGTGTGTCAA

FIGURE 182

MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFFQPPKRNWFWG
HLGLITPTEEGLKDSTQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLF
IRFLKPWLGEGILLSGGDKWSRHRRLTPAFHFNILKSYITIFNKSANIMLDKWQHASEGS
SRLLDMFEHISLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
LSHDGRRFHRACRLVHDFTDVIRERRRTLPTQGIDDFKDKAKSKTLD FIDVLLLSKDEDEG
KALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCQEVEQLLKDRDPKEIEW
DDLAQLPFLTMCVKESLR LHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW
PDPEVYDPFRFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHT
EPRRKLELIMRAEGLWLRVEPLNVGLQ

FIGURE 183

CAACAGAAGCCAAGAAGGAAGCCGTCTATCTTGTGGCGATCATGTATAAGCTGGCCTCCTGC
TGTTTGCTTTTCACAGGATTCTTAAATCCTCTCTTATCTCTTCCTCTCCTTGACTCCAGGGA
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCTTAACTCCGGAGGAGCTAGAAA
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTTTAACCCAAGAGGAAATTGAGAAAGTTTCAGGATTT
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTGGCCAGAATCTGGAACCATACA
AGAAACGTGAGACTCCTGATTGCTTCTGGAATACTGTGTCTGAAGTGAAATAAGCATCTGT
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACAATGCTTGATTGAAAAC
AGTGTGGAGAAAACTAGGCAAACACACCTGTTTCATTGTTACCTGGAAAATAAATCCTCT
ATGTTTGCACAAAAAAAAAAAAAA

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184/330

FIGURE 184

MYKLASCCLLFTGFLNPLLSLPLLDREISFQLSAPHEDARLTPEELERASLLQILPEMLGA
ERGDILRKADSSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRETPDCFWKYCV

184/330

FIGURE 185

GAACATTTTTAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
GGGGTTGCTGGTTTTAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA
CCACCTCCGCCAGGAAGTGCAGGCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCCCC
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT
CCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCCGGAAGATGGAGGTCAAGCAGA
AGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT
CAGGGGTTCAGTACCAGCAGCACAGCCAGGCCCTGGGGAAAGTTTCTTCAGGACATCCTCTGG
GAAGAGGCCAAAGAGGCCCCAGCCGACAAGTGATCGCCACAAGCCTTACTCACCTCTCTCT
AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTA
CAAGCTCAGGAGGCGAATAAATGTTCAAAGTGA

FIGURE 186

QUESTIONS

FIGURE 187

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCTCGTCCAGTACCTC
 GTGAACCCCGGGTGCTCCGCACGGACCCAGATGTCAAGAATATGAACACGTGGCTGCTGT
 TCCTCCCCTGTTCGCGTGCAGGTGCAGACCCTGATAGTCGTGATCATCGGGATGCTCGTG
 CTCCTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT
 GAGTATGTCCCCACCCTAAGCCCCGATCCCCCAAGCTGGGTGGTCAGAGCTGCTCATC
 TTACACCTCTACTTGAGTATGTCCCTAACCCTGAGCCCCCACGCCTGGGGCCAGAGTCTTT
 GTCCCCCGTGTGCGCATGTGTTTCAGGGTCAGCCTCTCCAGAAGTGAGATCATGGACAAAA
 GGGCAAATCACAGGAAGAAATTAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAAC
 TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAAAATGTTCAGA
 GACAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT
 CCAAAAACACAAGTAGAAATTTCTAACATGAAATATATTACAGGCAGGTACCCCACTAACCA
 AACAACTGAAGCGAGAGCTGTGGTCTTGCTTTGGTCTCACAGTGGGCACAGCGGTAGGCGGTC
 AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT
 AACAAACACCTCCCTGCTCCTGGCACCAGCCGTTTTTGGTCATGGTGGGCCAGCTGCAAAAGCG
 TCTTCCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGGTTTCTGTGGAC
 ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGATGCCCTGCTCCTGACAGCTTGGCCA
 ACCCTTGGTCAGGGCAGAGGGAGTTGGGTGGGTCAGGCTCTGGGCTCACCTCCATCTCCAGA
 GCATCCCTGCCTGCAGTTGTGGCAAGAAGCCCCAGCTCAGAATGAACACACCCCAACCAAGA
 GCCTCCTGTGTTACATAACCACAGGTTACCTTACAAACCACTGTCCCCACACAACCTGGGGAT
 GTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCTGAGGGTTGA
 ATTTTTTTTAAATGAAAGTGAATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA
 AAAAAAAAAAAAAAAAAAAAAAAAAA

MNTWLLFLPLFPVQVQTLIVVIIGMLVLLDFLGLVHLGQLLI FHIYLSMSP T LSPRSPQGW
VVRAAHLTPLLEYVPNPEPTPGARVVFVPRVRMCSGASPRSEIMDKKGKQSEI KSMRTQQ
AQQEAE LTPR PAGVVPGA

FIGURE 189

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACC**ATG**GCCAAAG
 ATGGAGCTCTCGAAGGCCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT
 ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG
 TGCCCAAGCCCCCTGTGCGAGAAAGGTCTGGCAGCCAAAGTGCTTTGACATGCCAGTGTCCCTG
 GATGGAGATACCAACACATCCACCCAGGAGGTGGTACAATAACAACCTGGGAGACTGGGGATGA
 CCGGTTTCTCCTTCCGGAGCTTCCGGAGTGCCATGTGGCTATCCTGTGAGGAAACTGTGGAAG
 AACCCAGGGGAGAGGTGCCGAAGTTTCATTGAACCTACACCACCAGCCAAGAGAGGTGAGAAA
 GGACTACTGGAATTTGCCACGTTGCAAGGCCCATGTACCCCCACTCTCCGATTTGGAGGGAA
 GCGGTTGATGGAGAAGGCTTCCCTCCCCTCCCCTCCCTTGGGGCTTTGTGGCAAAAATCCTA
 TGGTTATCCCTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTTCCTCCTGCT
 ACTAACAGACTTGCTACTACTGGGAACCCCTGCCTGTGGGCTCAAACCTGAGCGCCTTTGCTG
 CTGTTTCTCTGTCTGTCTCAGGTCTCCTGGGGATGGTGCCCCACATGATGTATTACAAAGTC
 TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGAATTTATGGCTG
 GGCTTCTACATGGCTGGCTCTCCTTCACTGCTGCATGGCGTCGGCTGTCAACCACCTTCA
 ACACGTACACCAGGATGGTGCTGGAGTTCAGTGCAAGCA**TAG**TAAAGACTTCAAGGAAAAC
 CCGAAGCTGCCTACACATCACCATCAGTGTTTCCCTCGGGCGGTGTCAAGTGCAGCCCCAC
 CGTGGGTCTTTGACCAGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGG
 GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGGAGCTG
 AAAGAAGCAGTTAGGTTCATCTGTAGAGGAAGAGCAGTGTAGGAGTTAAGCGGGTTTGGGA
 GTAGGCTTGAGCCCTACCTTACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG
 TCTCTTGAGCATGGTTTTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC
 CTAAGGGATTCTGGGTGCCACTGCTCTCTTTTCTCTACAGCTCCATCTTGTTTCAACCAC
 CCCACATCTCACACATCCAGAATTCCTTCTTTTACTGATAGTTTCTGTGCCAGGTCTGGGC
 TAAACCATGGAGATAAAAAGAAGAGTAAAATACACTTCCCGACCTTAAGGATCTGAAA

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MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFGVTQKVPKPLCEKGLAAKCFDMP
VSLDGDNTSTQBEVVQYNWETGDDRFSRFSRSGMWLSCETVEEPGERCSRFIETPPAKR
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLSPSPPLGLCGKNPMVIFGNADHLHRTSIHQL
PATNRLLAHTHWEPLQAOTERLCCFLCPVRSPGDDGGPHDVFSTLSPLSDCQLGSRRLTETCLE
LWLGLLHGLALLHLLHGVGCHHLQHVHQDGAGVQQA

FIGURE 191

AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCCA**GATG**TGGTTACCCCTTGGTCTCCTG
TCTTTATGTCTTTCTCCTCTTCTATTCTGTCATCTCCCTCACTTAAGTCTCAGGCCTGTCA
GCAGCTCCTGTGGACATTGCCATCCCTCTGGTAGCCTTCAGAGCAAAACAGGACAACCTATG
TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGT
GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG
AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCTGCCCTATTCTCCTCCCAA
GTCTGTTCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCAATGGCATTACAGAGAAAG
CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT
AGCCACCTCCCTGTGACCCAGTATTAACATGTCCCTTCCCCCTGCCCGCCGTAGATTGAG
GACATTGCCCCCTGTGTGCCACCAACCAGGACTTCCCCCTTGGCTTGGCATCCCTGGCTCT
CTCCTGGTACCAGCAAGACGTCTGTTCCAGGGCAGTGTAGCATCTTCAAGCTCCGTACT
ATGGCGATGGCCATGATGTTACAATCCCACTTGCCTGAATAATCAAGTGGGAAGGGGAAGCA
GAGGGAATGGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCTGAGGAAAAACCAAA
GGGAAGCAACAGGAACTTCTGCAACTGGTTTTTATCGGAAAGATCATCTGCTGCAGATGC
TGTTGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAA
ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATTCTGATTCCAAACCTCTTTATTACTTTGGG
AAGTCACTCAGCCTCCCCGTAGCCATCTCCAGGGTGACGGAACCCAGTGATTACCTGCTGG
AACCAAGGAAACTAACAATGTAGGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCC
CATGCCACCAAAACAATAAAACAAAATTCTCTAACACTGAAA

192/330

FIGURE 192

MWLPLGLLSLCLSPILSSPSLKSQACQQLLWTLPSPLVAFRANRTTYVMDVSTNQSGME
HRNHLCFCDLYDRATSPPLKCSLL

U988882.11149

FIGURE 193

GTAGCGCGTCTTGGGTCTCCCGGCTGCGCGTGTGCGCGCGCGCGCTCGGGTCTGGAGCCAGGAGCGAGCTCA
 CCGCGATGGCAGGCATCAAGCTTTGATTAGTTTGTCCCTTTGGAGGAGCAATCGGACTGATGTTTTTGTATGCTT
 GGATGTGCCCTTCCAATATACACAATACTGGCCCTCTTTGTCTATTTTTTACATCTTTCCACTTATTC
 ATACTGTCATAGCAAGAAGATTAGTGGATGATACAGACTGCTATGAGTAACGCTTGTAAAGAACTCCGATCTTTC
 TTACAACGGGCATTGTCTGTACAGCTTTTGGACTCCCTATTGTATTTGGCAGGACACATCTGATTGAGTGGGGGA
 GCTTGTGCACTTGTCTCAGGAAACACAGTCACTCTTTGCAACTATACTAGGCTTTTTCTTGGCTCTTGGAG
 CAATGACGACTTCAGCTGGCAGCAGTGGTGA¹AAAGAAATTAAGTCACTATTGTCAAAATGGAATTCCTGTCACTT
 GTTGGCCATTTCAGCACACAGGAGATGGGCGAGTTAATGCTGAATGGTATAGCAAGCCCTCTGGGGGTATTTTA
 GGTGCTCCCTTCTCACTTTTATTGTAAGCATACTATTTTCACAGAGACTTGTGAAGGATTAAGAGGATTTTCT
 CTTTTGGAAAAGCTTGACTGATTTTACACTTATCTATAGTATGCTTTTGTGGTGTCTGCTGAATTTAAATAT
 TTATGTGTTTTCTGTAGGTTGATTTTTTTTGAATCAATATGCAATGTTAAACACTTTTTTAATGTAATCA
 TTGCAATTGGTTAGGAATTCAGAATTCGCGCGGCTCTATTACTGGTCAAGTACATCTTTTCTCTTAAATATT
 TAGCCTCCATTATTACAAAAAATATAAAAAAATAGTTTTCACTGAGTCAAGTACATCTCCCAATGTTATG
 CAGACATACAGACGGTTGGCATACTATAGACTGTATACTCAGTGCAAAATATAGCTGCATTTATACCTCAGAG
 GGGCCAAAGTGTAATGCCATGCCCTCCGTTAAGGGTGTGTTGTTTACTGGTAGACAGATGTTTTGTGATTTG
 AAAATTAATTTATGGAATTCAGAGGAGTGGTTTTCTTCTCAATTTAGAGAATTTATGTTAAACTTTA
 AGGTAAGGGTGTAAACACTTTTGAGATAAGGTTTTTATTTATGTTTATTATTTGATAGTGAGTTGCAATGT
 GGGAGAAGATGACATTGAAATTCAGTTTTTGAATCCTGTTTTCTATTTATAAGTGAATTTGTGATCTCCTATC
 AACCTTTTATGTTTTTAACTGTAAATGGACATACATGGAACCACTACTGATGAGGGACAGTTGATGTTTGC
 ATCATATATGCCAGAAAACCTTCTCTGCTTCTTCTTTGACTTATTGGTATGTTGTATATATTACATAAAA
 TAACTTTTCAATATAGTTTATAACACTTGAAGTGTCTACTTACCTGAAAAATTAATGCTATGCCGTACATT
 CAGAGTGCCCTCCCTGCAAGGCCCTGCCATGATTAACAAGTAACTGTTAGTCTTACAGATAATTCATGCA
 TTAACAGTTTAAGATTAGACCATGGTAATAGTAGTTCTTATTCTCAAGGTTATATCATATGTAATTTAAAG
 TATTTTTTAAGACAAGTTTCTGTATACCTCTGAAGTGTGTTGATTTTGAAGTTCATCATAGATGCTGCTGTT
 CCTTATAAAGGCATTTGTTGTGTAGTTAATGCAAGTAGCCAAAGTCCAGCTATATAGCAGCTCAGAAACAT
 ACCTGACCAAAAAATTCAGTAAACAGGAGCATGATCAATTTATAGTGGTCTTTACATCTAATTAATATCAGGA
 CTTTTTTCAGAGTGGGTTATATAAAACATTCAAGTGGTCTGACAGTATTTTGTAAAGGATATTGTTTGTATG
 TTTATTCAGTATACCTTACATAAAAAATTTTCGCCATCAGCCAAACCTCAGTAATCAGACAGCTCTCTGTGT
 TTTATGAGGTTTATTCTCAAGAAAATGGGAATAAATTTGGGATTTGTTCAAGCTTTTTTACTAAAGATCCCTAA
 AGCCACAGGTTTTATTGGCTAACTTAAGCCATGACTTTTAGATATGAGATGACGGGAAGCAGGACGAAATATCG
 GCGTGTGGCTGGAGCCTTCCCACTGGAGGCTGAAGTGGCTTGTGCTATTATAATGTTCAAGTTTCAAGAGAA
 GGTGCAGGTACACATGAGTTAGAGAGCTGGTGAGACAGTTGGGAACCTTTTGTGCTGTGATCTACTGGAATTT
 TTTTTTGCAGGAAGTGCATTTCTCTGCTTCCCTATTCTTGTCTGGAATGTCAGTGCAGTGCAGTGCAGTCTG
 TTTTATCACTGGCCACAGACTTTTTCTAACAGCTGGGATTTATTTCTATATCAATTTGCAATGGCAGCATT
 GTGCTCTGACCTTGTATCTAGCTTGACATAGTCTGTCTGATTTCTAGGCTAGTTACTTGGAGATATGAAT
 TTTCCATGAATATGCATGATACACATTACCATTCTTCTATGGAAGAAAACCTTTTGTATGATGAACAAATAA
 AGATTTTTAAATATCTATTTTAAAAAATAA

FIGURE 194

DEPOSED BY

CACGGGTCGCGCCCAAGCTTCGCGCCACGGGTCCGCGACGGCTCGCGCCGCGCGCTCGCGCGCGGTCCGCG
 CAGGGTCGCGGTGACAGCTCGCGCGACATCTGCTGGTAGGGGAAGGAGCGCGCGCTCTCGCGCGCTCCG
 CGCGCGCGCTCCGCGACCTCCACCG
 TCTCGAGCTTGCCTGGCGCGCGAATGGCAGGCTGTTCGCGGAGTAAAGGTGGCGCGCGGTGAGTGGTCTTC
 CAATGACGACATTAACCGAGCTGTGCATAGTCTGGGAGTGCAGCGCCGAGTTTGGAGTTTTCCTCCCAAC
 AACGTCTGAGCTTCGAGCTCAGAGGGAAGAAGAGCGGAGGAGCGAAGCTCGGGCTCGGCGACGTAAGTGG
 GACGACATTTGGCGCGCTAGAGCTGCGCTCCCGCGCTTCGCGCGCGCGCTTCGAGCGCGCGCGAGCAGCAAGT
 GCG
 GCGCTGCTATAATTAAGTCTGCACACGGAGGACGACATTAAGAGCGCGCGCGCGCGCGCGCGCGCGCGCG
 GACCGAGCGCTTCCAATGGACATTTCCAGATCTCTGGAAGAAGATTCGCTCATATGTAATTCTCGCTCTCG
 CTCTGTCTATACTGGCTGTGAGGAGGCCCTCGGGGGTGGTCTGTGTCTGTGGGGCGCGTCTTCAGATGCT
 CGCCCGCGCGCGCGCGCGGTGGCGCGAGCTGTGCGGTGCGAGGGCGCGGTGTAGTACATGCGAGGCGCTCAAC
 TCACGACGCGCGCGCGACACCTCTCGCGCTCGGTGGGTCTGCTCGGTGCTGCGACAGCGCTCTCGAGTGTGC
 CGCGCGCGCGCGCGGTATGACGCTACGCTGCTCTATCTGGATACCAATACATCTGCTCGGTGCGAGGG
 GGACGCTCTGCAGAAATGCG
 CCGCCTTTCGGCGCGCTGCCAACCGCGCGCGGTGACCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
 CTCTCTCGCGCGCTCGCGAGGCTCACCAGCTCGATATCGGGCGCAACGCCATCGAGTTTGTGCCGCTCGCTAT
 TCTTCAGGACTCGCGCGCGCTCAAGTTTCTGCATCGATCGATCAATAGTCAAGAGTCTGGCGCGCAACTCTT
 TCGCGCGCTTGTTAAGCTCAGCGAGTGCACCTCGAGGACACAGCACTTGTCAGGTGAACTTTCGCCCACTTC
 CGCGCGCGCTGATCTCCGCGACTCTGTGCTCGGGAGGACACAGGTGGCCATTTGTGTGAGCTCGCTCGGACTG
 TGGCGCGCTGACATCTCGTCAAGGCTGTGCTGCGCGACGAGTTCGAGTTCAGATCGAGCGCGCGCATGTGCG
 AAGTCCCTGCAAGCATCACCTTGGCGGGGAACCTGTGGATTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
 GCTCGCACAACTTCAGGGGGCTCATGATGGCACTTTCGAGTGGCGCGCGCGCGGATGACGACAGGGCGAGGACG
 TCTGCGACGCGGTGTAGCGCTTCCACTTGTGCGAGATGGGGCGAGCCACAGCGCGCACCTGTCTCGCGCG
 GTCACCAACCGCGAGTGTCTGGGCGCGCTCGACGCTGGCCGACACGCTCGCGAGCGCGGGGAGGGGCGACG
 CGCGCGCGCGCGCGCGCGCGCGCGCGCTTTCAGCGGGCGGAGACCGCGAGACCGCGTGCAGATCCACG
 AGGTGCTGCGGGCG
 GTTTTCCGACCGCGCTCAGCGCAGCTCAGACAGTCTGTTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
 CATGTCATCAGTGGCTGCACTTCTGCGCGGAATACATGTTGATTACAACCGCAACCATTCAGGAGGACG
 TGTGATCATCAACGAGTATGGCTGTGCTATCTGCCACGACGACCGCGCGGGAATCGCAGGTGTGAATTCTCC
 CAGTGCGCTTCAACCGTTCGCTCAAAATACGCTTGGCGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGGT
 TCTCTGTCTGTGCTCTGATATGCTCTTGACTGAAACTTAAAGGGATCTCTCCGACGAGCTTGACATTTAG
 ATCTCTAAGTCTGGAATTCAGTCAACAAAGCGAATAAACACACAAACACCGCGCGCGCGCGCGCGCGCGCG
 TATCTTAAATTTATGTGCG
 AAGAGTGGCGATAGACGAGAGAGAGATTAATCTGCTTCTGTTTATCTATACGCGCGCGCGCGCGCGCGCG
 AACATGTGATTTGTAGAAGATCTTAAGTCCATAGCATTTCTATGAAGAACCATTGAAAGAGGAATCTCAACT
 TGGGAGCTTTAGAGCGAATGACATGACATAGAAAGCATGTCTTACTTTGTGTGTGTCTGTATTTCTGCT
 TTTGTGTCTTTGTAGCGAGCAAACTTTGTCTACACAAAGGGAATTTAGCTCATCATTTTATGCCCGTTGT
 ATCTCTAGTCTTGGAGTTCTGGGGGGAGCTGGGGGGAAGCGCGAGGAATAGGGGAAAGTGGTATTTAACT
 AAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT
 CCTCTAAGCAAACTATAAGCATTTAAAGAGATCTATTAATTAATTTAGTCTTACGAAACTTGCCTGACG
 CCGACGAGGGTCTTAATCTATTATGCTGTGCTATCTGGAAGAAGACTAAGCGCAACTTACGCTCTGCTCTG
 GGCATGTGTAGGTGTACCTTCACTTTGCTGACTTCCGAGCTGTTAAAGTTTACAGTGGTATTTAGGT
 TTTGGAATTTATATATAGAAGAAAGCTTTTTCACATGACAAATGACACTCTCACACAGCTTATGCCCTAGTA
 GCTTTTATGTTTGGACGAGGAGGACAGGTTTAAATGAGACCTCTCTCTGCTGCTACAGAAATAAGGAGT
 CG
 ACTACAAGCTTACATCGCGAAGCGAGGTTTAAAGTCTTCTCTGCTGCTTGAAGAGAGAGATGAGTGGAG
 TCTTCTTGAACCTCAAGTAGAAGCGCCCAACTCTTCTCTGCTGCTTGAAGAGAGAGATGAGTGGAG
 ATTTAGCATCAACACACATTTATGATATATGATATATGAGTAAATTCAGGCGGGCAATGCCATCTGTTATTTCCCGA
 AGTTTTCAGGCAAGTAGACACAGATCTCTGTGATAGTTAGGCGGCACTTGTGTTTCGGCTTATTTTGTGCGA
 CTGTGCGCAAGTTTGTATCGCTAGTCTCTGACATGGCCGAGTAGAAGAGGCGATGTATGATCATGATGAT
 CTCTGAGAGAGTCTGATGATCATCCCTCTCGACGAGAAATTAACAAGAACAGAAATATATCTTGTTTGG
 AGCAATGCTGAT
 GCTGATTTTGGGTCTGCCATGACAGATTCGAAATAAAGAGAAATAGCTAGATATGACCATATATGCTCT
 CTGAATATATTTAGATAGGTTTGAATGTCA

MDFLLLGLCLYWLRLRPSGVVLCLLGACFQMLPAAPSGCFQLCRCEGRLLYCEALNLTAPH
NLSGLLGLSLRYNSLSELRAQFTGLMQLTWLYLDHNHICSVQGDAPQLRRVKELTLSSNQ
ITQLPNTTFRMPENLRSDLSYNKQLALAPDLFHGLRKLTLTHMRANA IQFVPRVIFQDCRS
LKFLDIGYNQLKSLARNSFAGLFKLTTELHLEHNDLVKVNFAHFPRILSLSHSLCLRRNKVAIV
VSSLDWVWNLEKMDLSGNEI EYMEPHVFETVPHLQSLQLDSNR LTYIEPRILNSWKS L T S I T
LAGNLWDCCGRNV CALASWLSNFQGRYDGNLQCASPEYAQGEDVLDAVYAFHLCEDGA EPTSG
HLLSAVTNRSLDGP PASSATTLADGGEGQHDGT FE PATVALPGGEHAENAVQ I H K V V T G T M A
L I F S F L I V L V L Y S V S C F P A S L R Q C F V T Q R R K Q K Q K T M H Q M A M S A Q E Y Y V D Y K P N H
I E G A L V I N E Y G S T C H O O P A R E C E V

FIGURE 197

GTGCAAGGAGCCGAGGCGAG**ATG**GGCGTCCTGGGCCGGGTCTGCTGTGGCTGCAGCTCTGC
GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTCGCAGCCAA
CTGGAGCCAGAACCAGGACCCCGTGCGCCGGCGGCGCGCTTGAGTTCCCGCGGACAAGATGG
TGTCAGTCCTGGTGCAAGAAGGTCACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGGAA
CTCGTCTTGGCTTCAGGAGCCGGATTGCGCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG
CGCGGGCGAACCTGCCGTCTTCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT
GGCGCTCTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCGTGGCCTGCCGC
CACGACGACGTCTTCTTTCCGCCTAGTGCCTCCTTCCGCGTGGGGCTCGGCCCTGGCGCTAG
CCCCGTGCGTGTCCGCAGCATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG
CTGTTTTCTGGCGTCCCGCGCGGGCGCCTACGCTTCCACGGGCCGGCGCGCT**TGA**GCGTG
GGCCCCGAGGACTGCGCGACCCGTGCGGCTGCGTCTGCGGCAACGCGGAGGCGCAGCCGTG
GATCTGCGCGGCCCTGCTCCAGCCCCT

FIGURE 198

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLVQE
GHAUSDMLPLDGELVLASGAGFGVSDVGSHLDCGAGEPAVFRDSDRFSWHDPHLWRSDEA
PGLFFVDAERVPCRHDDVFFPPSASFRVGLGPGASFVRVRSISALGRTFTRDEDLAVFLASR
AGRLRFHGPALSVGPEDCADPSGCVCGNAEAQPWICAALLQP

[illegible]

200/330

FIGURE 200

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYLSFIP
FARDAVKKCFVCLA

200/330-2986660

[illegible]

FIGURE 202

MTSKFILVSFILAALSLSTTFSLQLDQQKVLVVSFDGFRWDYLYKVPTPHFHYIMKYGVHVK
QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEETPIW
ITNQRAHGTSGAAMWPGTDVVKIHKRFPHTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLY
WEDPDDMGHHLGPDSPLMGPFVISDIDKKLGYLIQMLKKAKLWNTLNLIIITSDHGMTQCSEER
LIELDQYLDKDHYYTLIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYN
SRIQPIIAVADEGWHLQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD
LYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYQTSTILLPGSVKPAEYDQEGSYPYF
IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

FIGURE 203

GGATTTTTGTGATCCGCGATTTCGCTCCACGGGCGGGACCTTTGTAACTGCGGGAGGCCACG
 GACAGGCCACCCTGCGGGGCGGGAGGCAGCCGGGTGAGGGAGGTGAAGAAACCAAGACGC
 AGAGAGGCCAAGCCCCCTTGCTTGGGTCACACAGCCAAAGGAGGCAGAGCCAGAACTCACAA
 CCAGATCCAGAGGCAACAGGGAC**ATGG**CCACCTGGGACGAAAAGGCAGTCAACCGCAGGGCC
 AAGGTGGCTCCCGTGAGAGGATGAGCAAGTTCTTAAGGCACTTCACGGTCGTGGGAGACGA
 CTACCATGCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGGAGG
 AGCAGCCACCACCCACACCACTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCCTGACGTTGCC
 CCTGCCCTTGGCCCCGACCCAGGGCCCCCTTGACTTCAGGGGCATGTTGAGGAACTGTT
 CAGCTCCACAGGTTTCAGGTCATCATCATCTGCTTGGTGGTTCTGGATGCCCTCCTGGTGC
 TTGCTGAGCTCATCTGGACCTGAAGATCATCCAGCCGACAAGAATAACTATGCTGCCATG
 GTATTCCACTACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCTTTAAATT
 ATTTGTCTTCCGCCTGAGTTCTTTCACCACAAGTTTGAGATCCTGGATGCCCGTCGTGGTGG
 TGGTCTCATTCATCCTGGACATTGTCTCCTGTTCCAGGAGCACAGTTTGAGGCTCTGGGC
 CTGCTGATTCTGCTCCGGCTGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGT
 TAAGACACGTTCAGAACGGCAACTCTTAAGGTTAAACAGATGAATGTACAATTGGCCGCCA
 AGATTCAACACCTTGAGTTCAGCTGCTCTGAGAAGCCCCCTGGAC**TGA**TGAGTTTGCTGTATC
 AACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT
 CACACAGCCACCGTGAAAGTCCTGGAGTAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAG
 CAGGCTGGCATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTA
 TCACCTTCAGATTACAAATCACACAGAGCATCTGCCTGTTTTCAATCACAGAGAACAAAACC
 AAAATCTATAAAGATATTCTGAAAATATGACAGAATTTGACAAATAAAGCATAAACGTGTA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 205

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCAGTGGAGACCCAGCAGGCCGCCAACAT
 GCTCTGTCTGTGCCGTGTAGCTGCCGGTTCATCGGGGAAGCCAGACCGAGTTCACGTACTTTG
 AGTCAAGAGGGGCTCCCTGCCGAGCTGAAGTCCATTTTCAAGCTCAGTGTCTTCTCATCCCTCC
 CAGGAATTTCTCCACTACCGCCAGTGAAGCAGAAAATTTGTACAAGCTGGAGATTAAGGACCT
 TGATGGGCAGCTAGACTTTGAAGAATTTGTCCATTATCTCCAAGATCATGAGAAGAAGCTGA
 GGCTGGTGTCTTAAGATTTTGGACAAAAGAATGATGGACGATTGACGCCGAGGAGATCATG
 CAGTCCCTGCGGAGCTTGGGAGTCAAGATATCTGAACAGCAGGCAAAAAAATTTCTCAAGAG
 CATGGATAAAAAACGCCACGATGACCATCGACTGGAACGAGTGGAGAGACTACCACCTCCTCC
 ACCCGTGGAAAAACATCCCCGAGATCATCTCTACTGGAAGCATTTCCAGTCTTTGATGTG
 GGTGAGAATCTAACGGTCCCGGATGAGTTCACAGTGGAGGAGAGGCGAGCGGGGATGTGGTG
 GAGACACCTGGTGGCAGGAGGTGGGGCAGGGGCCATCCAGAACCTGCACGGCCCCCTGG
 ACAGGCTCAAGGTGCTCATGCAAGTCCATGCTCCCGCAGCAACATGGGCTATCGTTGGT
 GGCTTCACTCAGATGATTCGAGAAGGAGGGCCAGGTCACTTGGCGGGGCAATGGCATCAA
 CTGCTCTCAAAATTTGCCCCGAATCAGCCATCAAATTCATGGCTATGAGCAGATCAAGCGCC
 TTGTTGGTAGTGACCAGGAGACTCTGAGGATTACGAGAGGCTTTGGCAGGGTCTTGGCA
 GGGGCAATCGCCAGAGCAGCATCTACCCAATGGAGGTCTGAAGACCCGGATGGCGCTGGCG
 GAAGACAGGCCAGTACTAGGAATGCTGGACTGCCCGCAGGAGGATCTGGCCAGAGAGGGGG
 TGGCGGCTCTACAAAGGCTATGTCCCCAACATGTGGGCTCATCCCCATGCCCGCAT
 GACCTTGAGTCTACAGAGCGCTCAAGAATGCTGGCTGCAGCATCTGCAGTGAAGCAGCG
 GGACCCCGGGCTGTTTGTGCTCTGGCCTGTGGCACCATGTCCAGTACCTGTGGCCAGCTGG
 CCAGCTACCCCTGGCCCTAGTCAGGACCCGGATCGAGGCCCAAGCTCTATTGAGGCGCT
 CCGGAGGTGACCATGAGCAGCCTCTTCAAAATATCTTGGCAGCAGGAGGGGCTCTGGGCT
 GTACAGGGGGCTGGCCCAACTTTCATGAAGGTCTCCAGGCTTGAGCATCAGCTACGCTGAG
 TCTACGAGAACCTGAAGATCACCTGGGCGTGCAGTCCGCGTGAAGCGGGGGAGGGGCCCGCC
 CGAGTGGACTCGCTGATCTTGGGCGCAGCCTGGGGTGTGCAGCCATCTATTCTGTGAATG
 TGGCAACACTAAGCTGTCTCGAGCCAAAGCTGTGAAAACCTAGACGACCCCGCAGGGGGT
 GGGGAGAGCTGGCAGGCCCAGGGCTTGTCTGCTGACCCAGCAGACCTTCTGTTTGTGTC
 AGCGAAGACCACGAGCATCTCTTAGGCTCAGGGTACGAGGCTCGGGCTCAGATGTGTAA
 GCGAGGACATTTTCTGCAAGTGCCTGCCAATAGTGAAGTGGAGCCTGGAGGCCGCTTAGT
 TCTTCCATTTTCACTTTGCAAGCAGCTGTTGGCCACGCCCCCTGCCTCTTGGTCTGCCGTGC
 ATCTCCCTGTGCCCTTCTGCTGCCTGCTCTGCTGAGGTAAAGTGGGAGGAGGGCTACAG
 CCCACATCCCACCCCTCTGCTCAATCCCATATCCATGATGAAGGTGAGGTACGCTGGCCT
 CCCAGGCTGACTTCCCAACCTACAGCATTGACGCCAACTTGGCTGTGAAGGAAGAGGAAAG
 GATCTGGCCTTGTGGTCACTGGCATCTGAGCCCTGCTGATGGCTGGGGCTCTCGGGCATGCT
 TGGGAGTGTGGCATGAGGGCAGTGGAGCACCATGTTTGAAGGCGAAGGGCAGAGCCTTTGT
 GTGTTCTGGGGGAGGGAAGGAAAAGGTGTTGAGGCGCTTAATTAATGACTGTTGGGAAAAGGG
 TTTTGTCCAGAGGACAGCCGACAAATGAGCGACTTCTGTGCTTCCAGAGGAAGACGAGG
 GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTTCTGAGCGCCTGGGGGTTCTGTGCAACC
 CCAGAGGGGCGCAGGGGACGAGCCACATTCACCTTGTGTCACTGTGGAACCTTGAACCTAT
 ATTTTGTATTTTATTGAACAGAGTTATGTCTTAACATTTTATATAGATTTGTTTAATTAATA
 GCTTGTCAATTTTCAAGTTCAATTTTTATTTCATATTTATGTTTATGTTGATTTGACTTCCC
 AAGCCCGCCAGTGGGATGGGAGGAGGAGAGAAGGGGGCTTGGGCGCTGCAGTCACAT
 CTCTCCAGAGAAATTCCTTTTGGGACTGGAGGCAGGAGGCCGAGGAGGAGGAGGAGGAGG
 GCTCGCTTCTTGGCAGGTTGGGGAAGGGCTTGGCCCGAGCTTAGGATTTCAAGGTTTGA
 CACTGTGAATTTGTGGTGGCGGGGGCTGGAGGAGAGGTTGGGGGCTGCTCGCTGCCCTCC
 CAGCCTTCTGCTGCCCTTCTTAAACATGCGCGCAACTGGCGACCTCAGGTTGCACTTCC
 ATTCCACAGAAATGACCTGATGAGGAATCTCAATAGGATGCAAGAGATGCAAGCAAAAT
 GTTATATATGAACATATACTGGAGTCGTCAAAAGCAAATTAAGAAAGAAATTTGGACGTTAG
 AAGTTGTCATTTAAGCAGCCTTCTAATAAAGTTGTTTCAAGCTGAAAAAAGAAAAA
 AA

FIGURE 206

MLCLCLYVPVIGEAEQTEFYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKD
LDGQLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEKILK
SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMW
WRHLVAGGGAGAVSRTCTAPLDRLKVLQVHASRSNNMGIVGGFTQMIREGGARSLWRGNGI
NVLKIAPESAIKFMAYEQIKRLVGSQETLRIHERLVAGSLAGIAIQSSIYPMEVLKTRMAL
RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNLQHYAVNS
ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFG
LYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 207

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCC**AT**
GGCTTCCTCGGGGAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAG
 CAATTGCACTCATCATTGGCTTTGGTATTTTCAGGGAGACATCCATCACAGTCACTACTGTC
 GCCTCAGCTGGGAACATTGGGAGGATGGAATCCTGAGCTGCACCTTTTGAACTGACATCAA
 ACTTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTtaggCTTGGTCCATGAGTTCA
 AAGAAGGCAAAGATGAGCTGTGCGAGCAGGATGAAATGTTGAGAGGCCGACAGCAGTGTTT
 GCTGATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGC
 TGGCACCTACAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATA
 AAAGTGGAGCCTTCAGCATGCCGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG
 CGGTGTGAGGCTCCCCGATGGTTCCCCAGCCACAGTGGTCTGGGCATCCCAAGTTGACCA
 GGGAGCCAACCTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACCTCTGAGAAATGTGACCA
 TGAAGGTTGTGCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAA
 AATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAAGCGGGAG
 TCACCTACAGCTGTAAACTCAAAGGCTTCTCTGTGTGCTCTTCTTTCTTTGCCATCAGCT
 GGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAA**TAA**TGTGCCTTGGCCACAAAAAG
 CATGCAAAGTCATTGTTACAACAGGGATCTACAGAATCTTACCACAGATATGACCTAG
 TTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGCTTGGAGTGAGCAACAAGAGCA
 AGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAA
 GACATATTAGAAGTTGGGAAAATAATTCATGTGAAGTACAGTGTGTTAAGAGTGATAAG
 TAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTACCT
 GGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTtagTTATATGTGCTG
 TAATGTTGCTCTGAGGAAGCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATTTCCA
 CAAATTAAGCTGTAGTATGTACCTTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGG
 GCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTATGATGCTTCCAAAGGTGCCT
 TGGCTTCTCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAA
 ACAGAGCAGTCGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAAAAA
 AA

MASLQGILFWSIISIIIIILAGATALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI
KLSDIVIQWLKEGVLGLVHEFKEGKDELSQDEMFGRGTAVFADQVIVGNASRLRKNVQLTD
AGTYKCYIIITSKGKGANLNEYKTGAFSMVNVVDYNASSETLRCEAPRWFPPQPTVVWASQVD
QGAFSEVSNSTFELNSENVMTKVVSLVNYTINNTYSMIENDIKATGDIKVTSEIKRR
SHLQLLNSKASLQCVSFAISWALLPLSPYLMLK

FIGURE 209

GAATTTGTAGAAGACAGCGGCGTTGCCATGGCGGCGTCTCTGGGGCAGGTGTTGGCTCTGGT
 GCTGGTGGCCGCTCTGTGGGGTGGCACGCAGCCGCTGCTGAAGCGGGCCTCCGCCGGCCTGC
 AGCGGGTTTCATGAGCCGACCTGGGCCCAGCAGTTGCTACAGGAGATGAAGACCCCTCTTCTTG
 AATACTGAGTACCTGATGCCCTTTCTCTCTCAACCAGTGTGGATCCCTTCTCTATTACCTCAC
 CTTGGCATCGACAGATCTGACCCTGGCTGTGCCCATCTGTAACCTCTCTGGCTATCATCTTCA
 CACTGATTGTTGGGAAGGCCCTTGGAGAAGATATTGGTGGAAAACGTAAGTTAGACTACTGC
 GAGTGGCGGACGCAGCTCTGTGGATCTCGACATACCTGTGTAGTTCTTCCCAGAACCCAT
 CTCCCCAGAGTGGGTGAGGACACGGCCCTTTTCCCATCTGCCCTTTCTCTGCAGCTGTTTT
 GCTTCCTTGTGGCCATCAGAGTTCCCTTCCCCTGGACAGCTGTGAGAAAAGACAGAGGCTGGG
 GTTGGGATTGAAGACCAGACCCCATCTGAGCCCTTCCCTCCAGCCCTGTACCAGCTCCTACT
 GGCATGGCTGAGCTCAGACCCTCCTGATTTCTGCCCTATATCCAGGAGCAGTTGCTGGCAT
 GGTGCTCACCGTGATAGGAATTCACCTCTGCATCACAAGCTCAGTGAGTAAGACCCAGGGGC
 AACAGTCTACCTTTGAGTGGGCCGAACCCACTTCCAGCTCTGCTGCCCTCAGGAAGCCCTT
 GGGCCATGAAGTGCTGGCAGTGAGCGGATGGACCTAGCACTTCCCCTCTCTGGCCTTAGCTT
 CCTCCTCTCTTATGGGGATAACAGCTACCTCATGGATCACAATAAGAGAACAAGAGTGAAAG
 AGTTTTGTAACCTTCAAGTGCTGTTGAGCTGCGGGGATTAGCACAGGAGACTCTACGCTCA
 CCCTCAGCAACCTTTCTGCCCCAGCAGCTCTCTTCTGCTAACATCTCAGGCTCCCAGCCCA
 GCCACCATTAAGTGGCCTGATCTGGACTATCATGGTGGCAGGTTCCATGGACTGCAGAACT
 CCAGCTGCATGGAAGGGCCAGCTGCAGACTTTGAGCCAGAAATGCAAACGGGAGGCCTCTG
 GGACTCAGTCAGAGCGCTTTGGCTGAATGAGGGGTGGAACCGAGGGAAGAGGTGCGTCGGA
 GTGGCAGATGCAGGAATGAGCTGTCTATTAGCCTTGCTGCCCAACCATGAGGTAGGCAG
 AAATCCTCACTGCCAGCCCTCTTAAACAGGTAGAGAGCTGTGAGCCCCAGCCCCACCTGAC
 TCCAGCACACCTGGCGAGTAGTAGCTGTCAATAAATCTATGTAACAGACAAAAAAAAAAAAA
 AA

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MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLLQEMKTTFLNTEYLMFPFL
LNQCSSLYYLTASTDLTLAVPICNSLAIIFTLIVKGALGEDIGGKRKL DYCECGTQLCGS
RHTCVSSFPEPISEWVRTRPFPILFPFLQFCFLVAIRVPFPWTVWRKTEAGVWD

FIGURE 211

CTTCTGTAGGACAGTCACCAAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG
GAAGATGACAGCAATTATAGCAGGACCCTGCCAGGCTGTCGAAAAGATTCCGCAATAAAACT
TTGCCAGTGGGAAGTACCTAGTGAAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT
TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACC**ATGA**AAGGGCATCCTCG
TTGCTGGTATCACTGCAGTGCTTGTGTCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAT
TCATGGGAAAAATCCTGTGTCAACAGCATTGCCCTCTGAATGTCCTTCACATGCCAACACCAG
CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT
TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCACGTGTCT
GCTGAAGAACACTTTTCATTTTGTAAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG
CGATGCCCTGGACCCTCCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTATG
AATCTAATGGAACCTTCCTGTCTGGGAAGCCCTGGAAATGCTATGAAGAAGAACAGTGTGTC
TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTT
CAACGTCAGTAACGCCACCTGTCTGAGTTCCTGTCTGGTGAACAAGACTCTTGAGGAGTCA
TCTTTCGAAAGTTTGAGTGTGCAAAATGTAAACAGCTTAACCCACAGTCTGCACCAACCACT
TCCCACAACGTGGGCTCCAAAGCTTCCCTCTACCTCTTGCCCTTGCCAGCCTCCTTCTTCG
GGGACTGCTGCCCT**TGA**GGTCTGGGGCTGCACTTTGCCAGCACCCCATTTCTGCTTCTCTG
AGGTCCAGAGCACCCCTGCGGTGCTGACACCTCTTTCCCTGCTCTGCCCCGTTTAACTGC
CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGTGCCTTGTCTTCTATTATTA
AAGCACTGGTTCATTCACTGCCAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 212

FOR THE PRESIDENT

FIGURE 213

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCA
GGGCTTGCCCTCACTGGCCACCCTCCCAACCCCAAGAGCCCAGCCCCATGGTCCCCGCCGCCG
GCGCGCTGCTGTGGGTCTGCTGCTGAATCTGGGTCCCCGGCGCGGGGGCCCAAGGCCTG
ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGCCCCATGACCCGCA
CTACCGGAGCACCGCCCGACTGGTCTTCCCCGGAAGACAAGGATAATCCTAGAGGACGAGA
ATGATGCCATGGCCGACGCCGACCGCTGGCTGGACCAGCGGTGCCGAGCTCTTGGCCGCC
ACGGTGTCCACCGGCTTTAGCCGGTCGTCCGCCATTACGAGGAGGATGGGTCTTCAGAAGA
GGGGGTGTGATTAATGCCGGAAGGATAGCACCAGCAGAGAGCTTCCAGTGCGACTCCCA
ATACAGCGGGAGTTCCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
ACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
CCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGGCCGTCAACCTCACCCACAG
CCATGCCATCTCCTGAGGATCTGCGGCTGGTGCTGATGCCCTGGGGCCCCGTGGCACTGCCAC
TGCAAGTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTTCCGGGCGCCT
TCGAGTTGGGGCGCTGAGCCAGCTCCGCACGGAGCACAAAGCCTTGACCTATCAACAATGTC
CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT
GCCTCTCAGAGCACCAACAGTACCAGGACCACCACTACCCCTTCCCCACCATCCACCTCAG
AAGCAGTCCCAGCCTGCCACCCGCGAGCCCTGCCAGCCCTGGCCTTTTGGAAACGGGTCA
GGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATA
GACAGAAACCAGAGGTAATGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCT
CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTTAGTACAGAAAAACAAAAGTGGAAAA
CACAA

214/330

FIGURE 214

MVPAAGALLWVLLNLGPRAAGAQGLTQTPTEMQRVSLRFGGPMTRSyrSTARTGLPRKTRI
ILEDENDAMADADRLAGPAAELLAATVSTGFSRSSAINeedGSSEEGVINAGKDSTSREL
PSATPNTAGSSSTRFIANSQEPEIRLTSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP
SPSPTAMSPEDLRLVLPWGPWHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQLRTEHKPC
TYQQPCPNRLREECPLDTSLCDTNCASQSTTSTRTTTTPFPTIHLRSSPSLPPASPCPALA
FWKRVRIGLEDIWNSLSSVFTEMQPIDRNQR

09090909-11011

FIGURE 215

CCCGGGTCGACCCACGCGTCCGGGGGAGAAAGGAATGCGCCGCTGGCGGCGCGGTTGGTCTGCTAGCTGGGGCA
 GCGGCGCTGGCGAGCGGCTCCAGGGGACCGTGAGCCGGTTACC GCGACTGCGTACTGCAGTGCAGAGAGCA
 GAACCTGCTCTGGGGGCGCTCTGAATCACTTCCGCTCCCGCAGCCAACTCTACATGAGTCTAGCAGGCTGGACCT
 GTCCGGGACGACTCTAAGTATGAGTGTATGTGGGTACCGGTGGGCTCTACCTCAGGAGAGGTACAAAGTGCCT
 CAGTTCCATGGCAAGTGGCCCTTCTCCGGTTCCTGTTCTTTCAAGAGCCGGCATCGGCCGTGGCCCTCGTGTCT
 CAATGGCTGGCCAGCTGGTGTATGCTCTGCCCTACCCGACCTCTGTCGCCAGCTCTCCCCCCGTATACACCA
 CCTGTGTGGCCTTCGCTGGGTGTCCTCAATGCATGGTCTATGTCACAGTCTCCACACCAAGGACCACTGAC
 CTCACAGAGAAATGGACTACTTCTGTGCCCTCCACTGTATCCTACACTCAATCTACCTGTGCTGCGTCAGGAC
 CGTGGGGCTCGACACCCAGCTGTGGTCAGTGCCCTCCGGGCTCTCCTGCTGCTCATGCTGACCGTGCACGTCT
 CCTACCTGAGCCTCATCCGCTTCGACTATGGCTACAACCTGGTGGCCAACTGGGCTATTGGCCTGGTCAACGTG
 GTGTGGTGGCTGGCCTGGTGCCTGTGGAACACCGCGGCGCTGCCCTCACGTGCGCAAGTGGCGTGGTGGTCTT
 GCTGCTGCAGGGGCTGTCCCTGCTCGAGCTGCTTGACTCCACCGCTCTCTGGGTCCTGGATGCCATGCCA
 TCTGGACATCAGACCATCCCTGTCCAGCTCCTCTTTTTCAGCTTTCTGGAAGATGACAGCCTGTACCTGCTG
 AAGGAATCAGAGGACAAGTTCAAGCTGGACTGAAGACCTTGAGCGAGTCTGCCCCAGTGGGGATCCTGCCCCC
 GCCCTGCTGGCCTCCCTTCTCCCTCAACCTTGAGATGATTTTCTCTTTTCAACTTCTTGAACCTGGACATGA
 AGGATGTGGGCCAGAAATCATGTGGCCAGCCACCCCTGTTGGCCCTCACCAGCCTTGGAGTCTGTTCTAGGG
 AAGGCTCCAGCATCTGGGACTCGAGAGTGGGCGAGCCCTCTACCTCTGGAGCTGAAC TGGGGTGGAACTGA
 GTGTGTTCTTAGCTCTACCGGGAGGACAGCTGCCGTGTTTCTCCACACAGCCTCTCCCCACATCCCAGCTG
 CCTGGCTGGGTCTGAAGCCCTCTGTCTACCTGGGAGACCAGGAGACCAGGCTTAGGGATACAGGGGGTCCC
 CTCTGTACACACCCCCACCTCTCCAGGACACCAGTGGTGGTGGTGGTCTGTTCTTTGGCCAGCCAA
 GGTTCACGGCGATTCTCCCATGGGATCTTGGAGGACCAAGCTGCTGGGATTGGGAAGGAGTTTCAACCTGACC
 GTTGCCCTAGCCAGGTTCCAGGAGGCTCACCATACTCCCTTTCAAGGCGAGGGCTCCAGCAAGCCAGGGCA
 AGGATCTGTGCTGCTGTCTGTTGAGAGCCTGCCACCGTGTGTGGGAGTGTGGGCCAGGCTGAGTGCATAGG
 TGACAGGGCCGTGAGCATGGGCTGGGTGTGTGTGAGCTCAGGCCAGGTGCGCAGTGGAGACGGGTGTTGT
 CGGGGAAGAGGTGTGGCTTCAAAGTGTGTGTGTGAGGGGGTGGGTGTGTAGCTGGGTAGGGGAACGTGTG
 TGCGGCTGCTGGTGGGCTGTGAGATGAGTGACTGCCGTGAATGTGTCCACAGTTGAGAGGTTGGAGCAGGAT
 GAGGGAATCCTGTCAACATCAATAATCACTTGGAGCGCCAGCTCTGCCCAAGACGCCACCTGGGCGGAGCAGC
 CAGGAGCTCTCCATGCCAGGCTGCTGTGTGCTGTTCCCTGTCTGGTGCCCTTTGCCCGCTCCTGCCAAAC
 CTCACAGGCTCCCAACAAAGTGCCTTCAGAAAGCAGCCCTCGGAGGACAGGGAAGGAAATGGGGATGGC
 TGGGGCTCTCCATCCCTCTTTCTCTCTGCTTCCATGGCTGGCCTTCCCTTCCAAACCTCCATTCCCT
 GCTGCCAGCCCTTTGCCATAGCTGATTTGGGGAGGAGGAAGGGCGATTGAGGGGAAGGGGAGAAAGCT
 TATGGCTGGGTCTGGTTCTTCCCTTCCAGAGGCTCTACTGTTCAGGGTGGCCCGAGGCGAGGGGCGCC
 ACATCTGCCTGTGCCCTGGTAAAGGTGACCCCTGCCATTTACCAAGCAGCTGGCATGTTCTGCCCAAGT
 AATAGATGAGGAGGAGCTCCAGAACTTTCCATCCCAAGCAGCTCCGCTGGTGAAGCAGACTGGATTG
 CTCTGCCCTGACCCCTGTCCCTCTTTGAGGAGGGGAGCTATGCTAGSACTCCAACTCAGGACTCGGGTG
 GCCTGCGCTAGCTTTTGTGATCTGAARCTTTAAGGTGGGAGGTGGCAAGGGATGTGCTTAATAATCAA
 TTCCAGGCTCAAAAAA

FIGURE 216

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSSGGALNHFRSRQPIYMSLAGW
TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPFSSRFLFFQEPASAVASFLNGLASLVMLCR
YRTFVPASSPMYHTCVAFAVWSLNAWFWSTVFHTRDLDLTKMDYFCASTVILHSIYLCCVR
TVGLQHPAVVSAFRALLLLMLTVHVSYSLSLIRFDYGYNLVANVAIGLVNVVWWLAWCLWNQR
RLPHVRKCVVVVLLQGLSLELLDFPPLFWVLDAHAIWHISTIPVHVLFFSFLEDDSLYLL
KESEDKFKLD

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

[illegible]

FIGURE 218

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPESSTKETERKETKAEEL
DAEVLEVFPHTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTN
TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
RLINKFNSSSSSLEEKIAALFDLEYVYVHQMDNAQDLLSFGGLQVVINGLNSTEPLVKEYAAF
VLGAAFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFYPYAQRQFLKL
GGLQVLRITLVQEKGEVLA VRVVTLLYDLVTEKMFEEEEAELTQEMSPEKLQQYRQVHLLPG
LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCRDRYRQDPQLGRITLASLQAEYQVLAS
LELQDGEDEGYFQELLGSVNSLLKELR

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

TTCCGGCTTCCGTAGAGGAAGTGGCGCGGACCCTCATTGGGGTTTCGGTTCCCCCCTTCCC
CTTCCCGGGGTTCTGGGGTGACATTGCACCGGCCCTCTGGTGGTTCGGTTGCCACCCCA
CGGGACATCCCCAGCTGGCGCGCCCTCCCATTTGGCTGTCTGGTGACGGCCCCACCCCC
TTCCACACCTGACACGAGC**ATG**GGGGCTGCGGTGTTTTTCGGCTGCACATTTCGTGCGTTCGGC
CCGGCCTTCGGCGCTTTTCTGGTCACTGTGGCTGGGAGCCCGCTTCGGTTATCATCTGGT
CGAGGGGACATTTTTCGGTGGTCTCCCTGCTCTGCCTCTGTGTTCTGGTTCATCTGGT
TCCATTGTACGACCGAGCTGCAGATGCCCGGCTCCAGTAGCGCCTCTGATATTTTGGTGTCTGG
GTCTCTGTCTTTACAGGAGGTGTTTCGCTTTGGCTACTACAAGCTGCTTAAGAAGGCAGA
TGAAGGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCGACATGGCCT
ATGTTTCTGGTCTCTCTCTCCGATATCATAGTGTGTCTTCTCTGTATCAATATTTTGGCT
GATGACATTTGGGCGAGGTGTGGTTGGGATCATGAGACTACCCCTATTACTCTGACATTC
AGCCTTTCTGACAGCAGCCATTATCTCTGCTCCATACCTTTTGGGGAGTGTGTCTTTGATG
CTCTGTGAGGAGGACCGGTACTTGGGCTTTGGGCGTGGTGTGGGAGTACCTCATGACATCTG
GGACTGCAATCTGAACCTCTGGTATGAGCCAGCTGCTGCCCACTCATGACGTACATGT
TTCCATGGGGCTCTGGGCCTTACCATACAGCTGAGGGGTCCCTCCGAAGTATTACGCGCAGCC
TTCTGTGTAAGGACT**TGA**CTACCTGGACTGATCGCTGACAGTCCCACCTGCCCTGCCCTGCTC
CCCATGACTGAGGCCAGCCCGAGCCGGGTTCATTGCCACATTTCTGCTCTCTCTCTGT
GGTCTACCCCACTACCTCTCAGGGTTTGTCTTGTGCTTTGTGACCGTTAGTCTCTAAGTCT
TACCAGGCGAGCTGGGTTCAGCCAGTCACTGAGTCTGGTGGGTTTGAATGCATCTATCCC
CACCACCTGGGACCCCTTGTGTGTCCAGGACTCCCCCTGTGTGAGTGTCTGCTCTCAC
CTCGCCCAAGACTACCTCCCTCCCTCTGCGAGCCGACGCGGAGGACATCGGGTGAT
GGTGATTCTGCCCTGCGCATCCACCCGAGGACTGAGGAACTAGGGGGGACCCCTGGGC
CTGGGGTGCCCTCTGATGTCTCGCCCTGATTTCCTCATCTCCGATTTCGGACAGTGAG
GTTGCCAAGAAAGGACCTAGTTTAGCCATTGCCCTGGGATGGAATTAATGGAGGCTCAA
GGATAGATGAGCTCTGAGTTTCTCAGTACTCCCTCAAGACTGGACATCTGGTCTTTTCTC
AGGCTCGAGGGGGAGCAACATTTTGTGTGATATAATACCTAACTGGGCTTTTCTCTTTT
GAGTGGGGGGAGGAGGAGGATTTAGGAATCTTCTAACCTCTGTGGCTTATATTTCCTC
TCCTCGAGTTGCTCTCATGGCTGGGCTCATTTTCGGTCCCTTCTCTCTGGTCCAGACCTT
GGGGGAAGGAAGGAAGTGATGTTTGGGAACCTGGCATCTGGAATCAATGGTTTAACTCT
CCTTAACACACGAGCATCCCTCTCTCCCAAGGTGAAGTGGAGGGTGCTGTGGTGAAGTGGC
GACTCCAGAGCTCGAGTGCCACTGGAGGATCAGACTACCGTAGGATCTGATGGGAGGAGGG
GAGATTTTTTTGTAGTTTAAATTTGGGTTGTGGAGGGCGGGAGGTTTCTATAAAGTGT
ATCATTTTCTGCTGAGGGTGGAGTGTCCATCCTTTAAACAAGGTGATGTGATTTTGAAT
ATAAAAAAAGAAATTTGTAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA
AAAAAATAAAAAAATAAAAAAATAAAAAA

MGAAVFVGCTFVAFGPAFALFLITVAGDPLRVIIIVAGAFFWLVSLLLASVWVILVHVTDR
SDARLQYGLLIIFGAASVLLQEVFRFAYYKLLKKADEGLASLSEGDGRSPISIRQMAYVSGLS
FGIISGVFSVINILADALGPGVVGIHGDSPPYFLTSAFLTAAILLHTFGWGVVFFDACERRR
YWALGLVVGSHLLTSGTLFNLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIORSLLCKD

AAGCTGGTTTAAGGAAGCAGAGGAGGGTTAGATTCTGTTGAGTGAGGACGGAAGATCAACCCA
 TTTCCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGTNT
 TNTCTGTTATCAATATTTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC
 TCACCCCTATTANTTCTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

FIGURE 222

GACCGACCGTTTCAGATGCCCGGTTCCAGTACGGCITTCCTGATTTTTGGTGCTGCTGTNTCTG
TCCTTCTACAGGAGGTGTTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTTCCATCCGCCAGATGGCCTATGTTTN
TGGTNTTTCCTTCGGTATCATCAGTGGTGTTTTNTCTGTTATCAATATTTGGNTGATGCAN
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCTATTAATTCCTGAATTCAGCCTTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTTGATGCCTGTGA
GAGGAG

NGTTGGAGAAAGTGGCGCGGACNNTTCATTTGGGGTTTCGGTTCCTCCCCCTTTCCCTTTCCCG
GGGTCTGGGTGACATTGCACGGGCCCTCGTGGGTGCGTGGCCACCCACGCGGACTCC
CCAGNTGGNGCGCCCTTCCCATTTGCTGTCTGGTCAGGCCCCACCCCTTCCACNTG
ACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTGCGTTCGGCCCGGCGCTTCG
CGCTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCTTGGTCGAGGGGCA
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTATCTTGGTCCATGTGAC
CGACCGGTGAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTCTGCTGTCTCTGTCC
TTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA
GCATCCTCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGG
TCTCCTCTCGGTATCATCGATGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACCTG
GGCCAGGTGTGGTGGGATCATGGAGACTACCC

GTAAAGAAAGTGGCGGACCTTCATTGGGGTTTCGGTTCCTCCCTTTCCCTNTCCCGGGG
TCTGGGGGTGACATTGCACCGCGCCCNCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC
CAGNTGGCGCGCCCTCCCATTTGCTGTCTGGTCAGGCCCCACCCCTTCCCACCTGA
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACTTTCGTCGCGTTCGGGCCCGGCCCTTC
GCGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCTCGTGCAGGGGC
ATTTTTCTGGCTGGTCTCCCTGCTCTGCGCTCTGTGGTCTGGTTTATCTTGGTCCATGTGA
CCGACCGGTGAGATGCCCGGCTCCAGTACGGCTCCTGATTTTTGGTGTCTGTCTCTGTCT
CTTCTACAGGAGGTGTTCCGCTTTCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGT
AGCATCGCTGATGTAGGAGCGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTG
GTCTCTCCTTTCGTTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTT
GGGCGAGGTGTGGTTGGGATCCATGGAGAC

CCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCCAGAGCCAGGAGGAGGCAT
TGGCCAGGAAGGCACAGGCCCTGAGAAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCC
TACCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGG
TGTCGTGCGTCTCTGCACCCACATCTTTCTCTGTGCCCTCCTTGCCCTGTCTGGAGGCTGCT
AGACTCCTATCTTCTGAATTCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCCG
CCTTGTGGTTCCTCTCTACCTGGGGAATAAGGTGCAGCGGCC**ATG**GCTACAGCAAGACCCC
CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTACAGAGCATGTT
CTCGCAACAATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA
GGACCTGGGAGCTGGGGCCGGGAAGACGCCCGGTGGATGACAGCAGCAGCCGCATCATCA
ATGGATCCGACTCGCATATGCACACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCCAAC
CAGCTCTACTGCGGGCGGTGTGGTGCATCCACAGTGGCTGCTCAGCGCCGCCACTGCAG
GAAGAAAGTTTTCAGAGTCCGTCTCGGCCACTACTCCTGTACCAAGTTTATGAATCTGGGC
AGCAGATGTTCCAGGGGTCAAATCCATCCCCACCCCTGGCTACTCCACCCCTGGCCACTCT
AAGCACTCATGCTCATCAAAGTGAACAGAAAGAAATTCGTCCCACTAAAGATGTCAGACCCAT
CAACGTCTCCTCTCATTGTCCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGACAA
CCAAGAGCCCCCAAGTGCACTTCCCTAAGGTCTCCAGTGCTTGAATATCAGCGTGCTAAGT
CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA
CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGCCCTGTGGTCTGCAATGGCTCCC
TGCAGGGACTCGTGTCTCTGGGGAGATTACCTTGTGCCCGGCCCAACAGACCCGGGTGTCTAC
ACGAACCTCTGCAAGTTCACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCT**TGA**GTGAT
CCCAGGACTCAGCACACCCGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTCAG
ACCCTCATTCCTTCCCAGAGATGTTGAGAATGTTTCATCTCTCCAGCCCCTGACCCCATGTCT
CCTGGACTCAGGGTCTGCTTCCCCACATTTGGGCTGACCGTGTCTCTCTAGTTGAACCTGG
GAACAATTTCCAAAATCTGCCAGGGCGGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTTCA
CTCAAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGACCCAATTTAGTCCCAGAAATAAA
CTGAGAAGTGGAAAAAAA

MATARFPMMWVLCALITALLGLVTEHVLANNDSVCDHPNSNTVPSGSNQDLGAGAGEDARSDD
SSSRRIINGSDCDMHTQPWQAAALLLRPNQLYCGAVLVPHPWLLTAAHCRKKVFRVRLGHYSLS
PVYESGQQMFQGVKSIPHPGYSHPGHSDNMLIKLNNRRIRPTDKDVRPINVSSHCPASGATKCL
VSGWGTTKSPQVHFPKVLQCLNISVLSQLRCKEDYNRPQIDMTFCAGDKAGRDSQCGSDGGP
VVCNGSLQGLVSWGDPACRNNRPGYNTLCKFTKWIQETIQANS

ATGTCGCAACGACCGGTGGGAAGACCATGGGCGCGCTGCCCAACTTGAGGACCGGCGCGCGCA
CAAGCGCGGACGGCGGAGCTCGGGCTACGTGCTCTGTGCACCGTCTGCTCTGGCCCTGGCTGTGC
TCTGGCTGTAGCTGTGCACCGTGGCGTCTCTCTGTAACACCGGCCGCGCGCGGACGAC
CGCGCTGCTGTGCTGTGCACCGGGGCTGTCTGACGCGCAACGCGCCCTGCTACTGTGTGA
AAGGCGCGACATCGCTGCTGACCGAGCTCTGCTGACCGGCTGCTGACGCTGCTGACGAC
GCTTCGACGCTGGAGAGCGCCGAGCGCTCGGTGTGACGAGCTGACGACGCGCGCGGCT
CAGCCACGCGCTGTGGGCGACGAGGACGAGAGCTGTGCACACGCTGGCGACGACGCTGCG
CCGGCTGCTGGCCGAGCCTCAGAGCTGCAGACCGAGTGTACTGGGGCTGGGAAAGGGGATC
GCACGCTGGGCGCGGCTCAGCGCCTCAGAGACTGAGCAGGCGCGCTCATTCAGCTCTCT
TCTGAGAGCCAGGGGACATGGCTCACTTGGTGAACCTCGTGACGACATCTCGTAGTGCCT
GCAAGGAGGACGGGGGCTGGGCGGGCCGCAACAGGCGCGACTTCAGAGAGGCGCTCGCC
GGGAAACCGGGCCGGGGCTGTGCCACTGGCTCCGCGCCGAGACTGTCTGAGACTCTCT
CTAAGCGGACGACGAGACGATGGCTCTACTCTGTCTTTCCACCCCACTACCGGCGGGCTT
CCAGTGTACTGTGACATPGCGACGAGCGCGCGGCTGGACGCTGTTTACGCGCCGGAGG
ACGGCTCCGTGAACCTTTCCCGGGCTGGGACGCGTACGAGACGGCTTTGACGAGCTCAC
GGGAGACATGGCTAGGCTCAAGAGGATCCACGGCTTACACACACAGGCTGCCATCAGCT
GCACGTGGACCTGGAGGACTTTGAGAAATGACACGGCCTTATGCCCGCTACGGGAGCTTCGGCG
TGGGCTGTCTTCCGTGGACCTTGAAGGAGCGGTTACCCGCTACCGTGGCTGACTATTCC
GGCATCGAGGCGATCCCTCTGAAGCACAGCGCATGAGGTTCACCAACAGGACGCTGTA
CAGCGACATTCAGAGAACTGATGCGCGCTTCTACCGGCTGTCCTGGTGGTACCGCAAT
GCCACAGCTCCCAACTCAATGGGAGTACTGCGCGGTGCGCGACGCTCTATGTCGCGAGCG
GTGAGTGTGCTCTCTGGACGGCTGGCACTGCTACCAAGTTCTCTGAGATGAAGATCCG
CGCGTTCGGGAGGAGCGCTAGATAGTGGTGAGTTGTCTTGGCCCTGCTGGTCTGCTGCG
CCCCCTCCCGACCCCACTCACTCTTTTCGTGAATGTTCTCCACCCCACTGTGCTGTGGCG
CCACTCTCCAGTAGGAGGAGGGCGGGGCCATCTCTTGACACAGAGCTCCTGGGCGGGTGAAGT
CACACATGCGCTTCTCGCGCTCCCCACCCCTCATTTGGCAGCTACTGATCTCTTGGCTC
TGCTGTATGGGGCTGGCAAACTTGACGCCAACCACTCTGCTGCCCCCACTGTGACTCCGG
TGCTGTTTGGCTCCCTCGCCAGGATGTTGGAGTGTGCCCCAGGACCCCTGTGCCCTGCC
GGCCAAATACCGGGCATTTAGGGAGCAGAGAGCAGGGGCGAGACAGCCCTTGAGTCTCT
CTAGCAAGATCGTGGGGAATGTGCGTCTCTTGAGGTCAAGTCTGAGGCCGCTGATCTCCAG
CCCTCCCAATGCCAACCCCAACCCGCTTTCCCTGGTGCGCCAGAGAACCCACTCTCCCCAA
GGGCTCAGCTGGCTGTGGGCTGGGTGGGCCCATCTTACAGGCGCTGAGGTCAAGATGGG
GAGCTGTGCTGCCCTTTGGGACCCAGCTCCAAAGGCTGAGACAGTTCCTCGAGGCGCCACCA
CTGTGCGCCGCGAGGCGCTGGGCTGTGAGTCTCTTACTGCTGTGCGGCTGCTCTCTG
TCTCAATGAGCGACCCATCTCCCCACCGAGCTCCGCGCGTCTCTCACTGGGGGAGC
CGGGGCTGCAATCCCAATCTTCTGCTCTTGGAAAGTTGGGTGGGGCTCAGCTTGGGGCT
GGAGCTGACCTTAATGGGAGGCTCTGGTTTGTCTGGGCTGGGGCTAGGACGGGCTGGGATGAG
GCTGTGACCTGCTCCACCAAACTTCCAGGGACTCAGGGTCTCTGAGGCTCCAGAGG
GCTGTGGGTGATGCTGCTGCTGAGGCTGCTGCTGATGAGGAGGCAACTCTGCTC
ATTGACGCTGGGCACTGGACCCAGGAGGAGGCTGCTGCTGATGAGGCTGCTGAGGACAG
CCACTCAGCGGCAAAATGGGTGGGGGAGGAGGAGGACGACGAGGCTGAGTGA
CTTTCTGTTGTAATCTCCCAACCGACGAGCTGTCACTCCCACTCTTGTGTGACACA
TGCAGAGGTTGAACCCGAGGCTCCAGGACAGCAGGCAACAGGGGAGGGCTGAGCGGG
TCTCAGCTGTCTGCTCAGCGCTCGGACGCTGCTGCTTACTGCTAGGCGCGATGCAAGG
CGGCTTTTCAAGCGCTCTGATGGGGCTCCGAAAGGGCTGGAGTCAAGCTTGGGGAGCT
GCTTAGCGGCTCTCTCGGCGAGGAGGGGAGGTGCTTCTTCCAAAGACACCGGATGCGA
GGTCCCTAGGGGGTGTGGGTTTCGTTTCTCCCTTCCCTCCAATGAAGTTTGTGCTAAAA
AACAATAAATGACTTGGCCACATCGGGGGTTGGTGGGAGAGGCGGTGTGACCTGGCTCT
TGTCAGGATGCCAACAGGTATCCACATCGCGAG

FIGURE 228

MVNDRWKTMGGAAQLEDPRDKPQRPSCGYVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT
APPPVVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALTEHQA
QPRLVGDQEQLLDTLADQLPRLRARASELQTECMGLRKGHGTLGQGLSALQSEQGRLIQLL
SESQGHMAHLVNSVSDIILDALQRDRGLGRPRNKADLQRAPARGTRPRGCATGSRPRDCLDVL
LSGQQDDGVYSVFPHTYPAGFQVYCDMRTDGGGWTVFQRREDGSVNFFRGWDAYRDGFGRLT
GEHWLGLKRIHALTTQAAVELHVDLEDFENGTAIARYGSFGVGLFSVDPEEDGYPLTVADYS
GTAGDSLKKHSGMRFTTKDRSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLRGAHASYADG
VEWSSWTGWQYSLKFSEMKIRPVREDR

FIGURE 229

GCAGTCAGAGACTTCCCCTGCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCT
 TGCTTCCCTGAAGTAGCTCACAGTAGCCCGCGGCCAGGGCAATCCGACCACATTTCACTCT
 CACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCAGGAGGACATGCTGGATGATG
 ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCC
 CGGCGCACAGAGCAGAGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCTGCTGAC
 TTTGTGCTTGGTGTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTACTACC
 AGCTCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATACGTCC
 CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCGAAGTCTGCAGCATGTGGC
 TGAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAG
 AACAAATGGAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAG
 GACTGTAAATATTTCTGCCTTAGTGAAACTCTACCATGCTGAAGATAACAACAAGAAGA
 CCTGGAATTTGCCCGCTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTTGGACAGGGCTTT
 TGGCCCTGACAGTGGCAAGGCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAACTG
 TTCCATATTATAATAGATGTCACCAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGG
 GATGATCTTCTCAAAGGACTGCAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAA
 TGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGTATTCCGC
 CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACAT
 TGGGAAATGGAACATAATCAGGAAAGACTATCTCTGACTAGTACAAAATGGGTTCTCGTG
 TTTCTGTTCCAGGATCACCAGCATTCTGAGCTTGGGTTTATGACGATTTTAAACAGTCA
 AGAAGTCTTATTTACATGCCACCAACCAACCTCAGAAACCCATAATGTATCTGCCTTCTTG
 GCTTAGAGATAACTTTTAGCTCTCTTCTCTCAATGTCTAATATCACCTCCCTGTTTTCAT
 GTCTTCTTTACACTTGGTGAATAAGAACTTTTTGAAGTAGAGGAAATACATTGAGGTAAC
 ATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATGGCAGTCACTTCCAGATTGTACC
 AGCAAATACACAAGGAATCTTTTTGTTGTTTTCAGTTCATACTAGTCCCTTCCCAATCCAT
 CAGTAAAGACCCCATCTGCCTTGTCCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAG
 AATCTCAAATCTCAATGCCCTTATAAGCATTCTTCCCTGTGCCATTAAAGACTCTGATAATTG
 TCTCCCTCCATAGGAATTTCTCCAGGAAAGAAATATATCCCATCTCCGTTTCATATCAG
 AACTACCGTCCCCGATATTCCTTCAGAGAGATTAAAGACCAGAAAAAGTGAGCCTCTTCA
 TCTGCACCTGTAATAGTTTCAGTTCCTATTTCTTCCATTGACCCATATTTATACCTTTCAG
 GTACTGAAGATTTAATAATAATAAATGTAAATACTGTGAAAAA

230/330

FIGURE 230

MQAKYSSTRDMLDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTCLVLL
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE
LYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAAS
QSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSRSDRCVAILNGMIFSKD
CKELKRCVCERRAGMVKPESLHVPPETLGEGD

U33333.1101
10011.233333

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCAGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTTCGGCATCCAG
AGCCCCGGCGCACAGAGCACAGGGNCTCTTTTCAACGTGGCGACCAGTGGCCCTGACCCGTG
CTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATA
CGTCCCAAGAGTTGCAATTNTTCAAGTCAGGAATAAAGCTTGCAGGAAGNTGCAGCAT
GTGGCTGAAAAACTCTGTCTGAGCTGTATAACAAGCTGGAGGAACCTTTGAAGGAGGGCAA
AGTNTCCCTCATNTACTATACACACCACTCTCC

FIGURE 232

GCCGAGCGCAAGAACCTGCGCAGCCAGAGCAGCTGCTGGAGGGGAATCGAGGCGCGGCTC
 CGGGGATTTCGGCTCGGGCCGCTGGCTCTGCTCTGCGGGGAGGAGCGGGCCCGCCCGGGG
 CCCGAGCCCTCCGGATCCGCCCTCCCGGTCGCCGCCCTCGGAGACTCTCTGGCTGCT
 CTGGGGGTTCCGCGGGGCGGAGCCGCGGTCGCGGGCGCC**CAT**GCGGCGATCGCTGCTGCTG
 TCGGTGCTCGGGCCCGCAGGGCCCGTGGCCGTGGGCATCTCCCTGGGCTTCACCTGAGCCT
 GCTCAGGCTCACTGGTGGAGGAGCCGTGCGGCCAGGCCGCCCAACTGGAGACTCTG
 AGTGGCGCCCGCGGCAACACCAACGCGCGCGCCGGCCCACTCGGTGCAGCCCGGAGCG
 GAGCGCGAGAAGCCCGGGCGCGGAAGCGCCGGGGAGAAATTGGAGCGCCGCGCTCTTGCC
 CTACCACCTGCACAGCCCGGCGAGGCCGCCAAAAGGCCGTGAGGACCCGCTACATCAGCA
 CGGAGCTGGGCTCAGGCAGAGGCTGCTGGTGGCGGTGCTGACCTCTCAGACACGCTGCC
 ACCTGGGCGTGGCCGTGAACCGCAGCTGGGGCACCGGCTGGAGCGTGTGGTGTCTCTGAC
 GGGCGCACGGGGCCCGGGGCCACCTGGCATGGCAGTGGTGACGCTGGGCGAGGAGCGAC
 CCATTGGACACCTGCACCTGGCGCTGCGCCACCTGGCTGGAGCAGCACGGCGACCACTTTGAC
 TGGTTCTTCTGGTGCCTGACACCACTACACCGAGGGCGCACGGCTGGCAGCCCTAACTGG
 CCACCTCAGCCTGGCTCCGCGGCCACCTGTACTGGGCGGCCCGAGGACTTCATCGGCG
 GAGAGCCCACTCCCGGCCCTACTGCCACGGAGGCTTTGGGGTGTGCTGTGCGCGCATGCTG
 CTGCAACAACCTCGGCCCACTGGGAAGCTGCGCAACGACGCTGCTAGTGGCGGCCCTGA
 CGAGTGGCTGGGTGCTGCACTTCGATGCCACCGGGTGGGCTGCACTGGTGACCAGGAG
 GGGTGCATATAGCCATCTGGAGCTGAGCCTGGGAGGCCAGTGACAGGAGGGGACCTCAT
 TTCCGAAGTGCCCTGACAGCCACCTGTGCGTGACCTGTGCACATGTACACATGCGACAA
 AGCTTTGCGCCGAGCTGAAGTGAACGCACGTACACAGGAGATCCAGGAGTTACAGTGGGAGA
 TCCAGAATACAGCCATCTGGCCGTTGATGGGGACCGGCGAGCTGCTTGGCCCGTGGGTATT
 CCAGCACCATCCCGCCCGGCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTCACGGAGCA
 GCACGCTTTCTCTGCGCGGATGGCTCACCCCGCTGCCACTGCGTGGGGCTGACCGGGCTG
 ATGTGGCCGATGTTCTGGGGACAGCTCTAGAGGAGCTGAACCGCCCTACACACCGGCCCTTG
 CGCTCCAGAAGCAGCAGCTGGTGAATGGCTACCGACGCTTTGATCGGCCCGGGGTATGGA
 ATACACGCTGGACTTGCAGCTGGAGGCACTGACCCCCAGGAGGCCCGCGGCCCTCACTC
 GCGGAGTGCACTGCTCCGGCCGCTGAGCCGCGTGGAGATCTTGCTGTGCCCTATGTCACT
 GAGGCTCACGTCTCACTGTGCTGCTGCCCTTAGCTGCGGCTGAGCGTGACCTGGCCCCCTGG
 CTTCTTGGAGGCCTTTGCCACTGCAGCACTGGAGCCCTGGTGATGCTGCGGCAGCCCTGACCC
 TGCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCGTGCCCATGCAGATGCTTTCGACCT
 GTCAGGCCCCAGCTGGCAGAGCTGGAGCGCGCTTCCCGGTGCCCGGTTGCCATGGCTCAG
 TGTGCAGACAGCCGACCTCACCCTGCGCTCATGGATCTACTTCCAAGAAGCACCCGCG
 TGGACACACTGTTCTGCTGGCCGGGCGAGACAGGTGCTCAGCGCTGACTTCTGAACCCG
 TCGCGCATGCTGCTGCTGCGGCTGGCAGGCTTCTTCCCATGCACTTCCAAGCTTCCA
 CCCAGGTGTGGCCCCACCAAGGGCTTGGGCCCCAGAGCTGGGCGGTGACACTGGCCGCT
 TTGATCGCCAGGCAGCCAGGCGGCTGCTTCTACAACCTCCGACTACGTGGCAGCCCGTGGG
 CGCTGGCGGCGAGCTCAGAACAAAGAAGAGGAGCTGCTGGAGAGCTGGATGTGTACGAGCT
 GTTCTCTCACTTCTCCAGTCTGCATGTGCTGCGGGCGGTGGAGCCGGCGCTGCTGCAGCGCT
 ACCGGCCCGAGAGCTGCAGCGCAGGCTCAGTGAGGACCTGTACCCAGCTGCTCCAGCT
 GTGCTTGAGGGCGCTCGGCTCCCGAACCAGCTGGCCATGCTACTCTTTGAACAGGAGCAGGG
 CAACAGCACT**CGA**CCCCACCTGTCCCGTGGGCGGTGGCATGGCCACACCCACCCACTCT
 CTCCCCAAAACAGAGCCACCTGCCAGCCTCGCTGGGCAGGGCTGGCCGTAGCCAGACCCC
 AAGCTGGCCACTGCTCCCTCTCTGGCTCTGTGGGTCTTGGGCTCTGACAAAGCACTGGG
 GGACGTGCCCCCAGAGCCACCACTTCTCATCCAAACCCAGTTTCCCTGCCCCCTGACGCT
 GCTGATCGGGCTGTGGCCCTCCACGTAATTTATGCAGTACAGCTGCGCTGACGCCAGCCCTG
 CTTGGGCCCTGGGGCTGGGCTGTAGAAGAGTTGTGGGGAAAGAGGAGCTGAGGAGGGG
 GCATCTCCCAACTTCTCCCTTTTGGACCCCTGCCGAAGCTCCCTGCCTTTAATAAACTGGCCA
 AGTGTGGA AAAA

FIGURE 233

MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELPFRGNTNAARRP
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAACKAVRTRYISTELGIRQLLVAVL
TSQTTLPTLGVAVNRTLGHRLERVVLTGARGRRAPPGMAVVTLGEERPIGHLHLALRHLL
QHGDDEFDFFLVPDTTYTEAHGLARLTGHLSLASAAHLYLGRPQDFIGGEPTPGRYCHGGFG
VLLSRMLLQQLRPHLEGCRNDIVSARPDDEWLGRCILDATGVGCTGDHEGVHYSHLELSPGEP
VQEGDPHFERSALTAPVRDPVHMYQLHKAFARAELEPTYQEIQELQWEIQNTSHLAVDGDRA
AAWPVGI PAPS RPASRFEVLRWDYFTEQHAFSCADGSPRCPLRGADRADVADVLGTAEELN
RRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALTPQGRRPLTRRVQLLRPLSRVEI
LPVPYVTEASRLTVLLPLAAERDLAPGFLEAFATAALEPGDAAAALTLLLLYEPRQAQRVA
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPLRLMDLLSKKHPLDTLFLLAGPDTVL
TPDFLNRCRMHAISGWQAFFPMHFQAFHFGVAPPQGGPPELGRDTRGRFDRQAASEACFYNS
DYVAARGRLAAASEQEEELLES LDVYELFLHFSSLHVLRAVEPALLQRYRAQTCSARLSEDL
YHRCLQSVLEGLSRTQLAMLLFEQE QGNST

FIGURE 234

GCTCTGGCCGGCCCCCGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT
TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCTTAGTGGAGAAAAGGAGT
AGCTATTAGCCAATTCGGCAGGGCCCGCTTTTGTAGAAGCTTGATTTCCTTTGAAGATGAAAG
ACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGGAACCTCGGGGCGATTGGCTGGGAA
CTGTATCCACCCAAATGTACCGATTTCCTCCTATGCAGGAAATGAGCAGACCCATCAATAA
GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACCTGGAGGCAAAG
AGGGTTGCTCAACGCCCCGCCTCATTGGAAAACCAATCAGATCTGGGACCTATATAGCGTG
GCGGAGGCGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTCT
TTCCCCGCCCTGAGACCTGCAGCACCATCTGTC**ATG**GCGGCTGGGCTGTTTGGTTTGAGC
GCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGCTCCCGCCGCCCGCGTCCGCTGGGA
ATCTAGCTTCTCCAGGACTGTGCTCGCCCGTCCGCTGTGGCGGAAAGCGGCCCCAGAAC
CGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACCTGTATGAGAAGAACCCA
GACTCCCATGGTTATGACAAGGACCCCGTTTGGACGCTCTGGAACATGCGACTTGTCTTCTT
CTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACCTTTGTGGCTATCTGCCTGACTACA
GGATGAAAGAGTGGTCCCGCCGGAAGCTGAGAGGCTTGTGAAATACCGAGAGGCCAATGGC
CTTCCCATCATGGAATCCAACGTGCTTCGACCCAGCAAGATCCAGCTGCCAGAGGATGAG**TG**
ACCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATTCTGAC
CTCTTCTCAGAGCACCTAATTAAAGGGGCTGAAAGTCTGAA

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MAAGFLGLSARRLLAAAATRGFLPAARVRWESSFSRTVVPASAVAGKRPEPETTPWQEDPEPE
DENLYEKNPD SHGYDKDFVL DVNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAER
LVKYREANGLPIMESNCFDPSKIQLPEDE

FIGURE 236

GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCTTTTGGCGGCAGCGGCACGCGAGGGC
TCCCGGCCGCCGCTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT
GTGGCGGGAAGCGGCCCCAGAACCGACCACACCGTGCCAAGAGGACCCAGAACCCGAGGA
CGAAAAC TTGTATGAGAAGAACCAGACTCCCATGGTTATGACAAGGACCCCGTTTGGACG
TCTGGAACATGCGACTTGTCTTCTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACC
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCT
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAAC TGCTTCGACCCAGCA
AGATCCAG

FIGURE 237

GCGGCGGCT**ATG**CCGCTTGCTCTGCTCGTCTGTTGCTCCTGGGGCCCGCGGCTGGTGCCT
 TGCAGAACCCACGCGACAGCCTGCGGGAGGAACCTGTCATCACCCCGCTGCCTTCGCGGG
 ACGTAGCCGCCACATTCCAGTTCGCGACGCGCTGGGATTCCGAGCTTCAGCGGGGAGGAGTG
 TCCATTACAGGCTCTTTCCCAAAGCCCTGGGGCAGCTGATCCAAAGTATCTCTACGGGA
 GCTGCACCTGTCTATTCACACAAGGCTTTTGGAGGACCCGATACTGGGGGCCACCCCTTCTGCTG
 AGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCCAAGACACTGTCACGTGATGTGGATAAA
 TCTTGGGAAGGAGCTCAGTAATGTCCTCTCAGGGATCTTCTGCGCCTCTCTCAACTTCATCGA
 CTCACCAACACAGTCACTCCCACTGCCTCCTTCAAACCCCTGGGTCTGGCCAATGACACTG
 ACCACTACTTTCTGCGCTATGCTGTGCTGCCGCGGAGGTGGTCTGCACCGAAAACCTCACC
 CCTGGAAGAAGCTCTTGCCCTGTAGTTCCAAGGCAGGCCCTCTCTGTGCTGCTGAAGGCAGA
 TCGCTTGTTCCACACCAGCTACCACTCCAGGCAGTGCATATCCGCCCTGTTTGCAGAAATG
 CACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCTGTCAGTTGTATTTGATGCCTTC
 ATCAGGGGGCAGGGAAGAAAGACTGGTCCCTCTTCCGGATGTTCTCCGAACCCCTCACGGA
 GCCCTGCCCTTGCTTCAGAGAGCCGAGTCTATGTGGACATCACCACTTACACCAGGACA
 ACGAGACATTAGAGGTGCACCCACCCCGACCACTACATATCAGGACGTATCCTAGGCACT
 CGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATCAACAACCTCTCGAAACCT
 CAACATCCAGCTCAAGTGGGAAGAGACCCCGAGAGAAATGAGCCCCCAGTGCCCTTCTCTGC
 ATGCCAGCGGTACGTGAGTGGCTATGGGTGCGAGAAAGGGGAGCTGAGCACACTGCTGTAC
 AACACCCACCCATACCGGGCCCTTCCCGGTGCTGCTGCTGGACACCGTACCTGGTATCTGCG
 GCTGTATGTGCACACCCCTCACCATCACCTCCAAGGGCAAGGAGAACAAACCAAGTTTACATCC
 ACTACAGCCTGCCAGGACCGGCTGCAACCCACCTCCTGGAGATGCTGATTGAGTGCCTGCG
 GCCAACTCAGTCACCAAGGTTTCCATCCAGTTTGAGCGGGCGCTGCTGAAGTGGACCGAGTA
 CAGCCAGATCCTAACCATGGCTTCTATGTCAGCCCATCTGCTCAGCGCCCTTGTCGCCA
 GCATGTAGCAGCCAAGCCAGTGGACTGGGAAGAGAGTCCCTCTTCAACAGCCTGTTCCTCA
 GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGAGCCGCTGCTGGTGAACCTGCC
 GACACCGGACTTCAGCATGCCCTACAACGTGATCTGCCTCAGTGCACGTGTTGGTGGCCGTGT
 GCTACGGCTCCTTCTACAACTCTCTCACCCGAACCTTCCACATCGAGGAGCCCCGCACAGGT
 GGCTTGCCCAAGCGCTGCCCCAACCTTATCCGGCGCGCCCCGAGGTGTCCCCCACTCT**GGA**TT
 CTTGCCCTTTCCAGCAGCTGCAGCTGCCGTTTCTCTCTGGGAGGGGAGCCCAAGGGCTGTT
 TCTGCCACTTGCTCTCTCAGAGTTGGCTTTTGAACCAAGTGCCCTGGACAGGTCAAGGC
 CTACAGCTGTGTTGTCCAGTACAGGAGCCACGAGCCAAATGTGGCATTGAATTTGAATTTAA
 CTTAGAAATTCATTTCCTCACCTGTAGTGGCCACCTCTATATTGAGGTGCTCAATAAGCAAA
 AGTGGTCGGTGGCTGTATTTGGACAGCACAGAAAAAGATTTCATCACCACAGAAAGGTC
 GGTGCGCAGCACTGGCCAAAGGTGATGGGTGTGCTACACAGTGTATGTCACTGTGTAGTGA
 TGGAGTTTACTGTTTGTGGAATAAAACCGCTGTTTCCGTGGAAAAA

MPLALVLVLLLPGGWCLAEPPRDSLREELVITPLPSGDVAATFQFRTRWDSLELQREGVSHY
RLFPKALGQLISKYSLRELHLHSFTQGFWRTRYWGPPFLQAPSGAELVWVFQDVTVDVDSWK
ELSNVLSGIFCASLNFDISTNTVPTASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCNRARCTSIISWELRQTLVSVPDAFITG
QGKDDWSLFRMFRTLTPECPPLASESRVYVDITTYNQNETLEVHPPTTTYQDVILGTRKT
YAIYDLDDTAMINNSRNLNIQLKWKRPPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH
PYRAFPVLLLDTPVWYLRLYVHTLTITTSKGKENKPSYIHYQPAQDRLOPHLEMLIQLPANS
VTSYISQIFERALKLWTEYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSD
GKNSVFRVLYTEPLLNVLTPTDFSPMPYVICLTCTVVAVCYGSFYNLLTRTFHIEEPRTGGLA
KRLANLIRRARGVPL

FIGURE 239

CAAC**ATG**GGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCTGGTGG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTGCCAGCTGACAACGTACGC
TGCTTCAAGTCCGATCCTCCCCAGTGTACACAGACCAGGACTGTCTGGGGAAAGGAAGTG
TTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCTGTGAAGGAAGTGAAGAAGGAGGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC
TCCTCCTCTACCAGGTGTCTCAGAA**TGAT**GTCTGGGTCCCTTCTACCTCTGGGGGTCACTC
TCACTTGGCACCTGCCCCTGAGGGTCCTGAGACTTGGAATATGGAAGAAGCAATACCCAACC
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTTTCCCCAAAAAGAGGGAAGAGTCACAAAAG
TCCAGACCCAGGGACGGTACTTTCCTCTCTACCTGGTGTCTCCTCCTAATGCTCATGAAT
GGACCCCTCATGAATGAAACCAGTGCCTTATAAGAGACCCCAAAGAGCTGCCTTGGCCCTTC
TGCAATGTGTGATCACAGCTAGAAGGCACTGTGAGAGAAGAGAACTGGTCCTCACCAGATG
CTGAATCTGCTGGTGCCTTGATCTTGGACTTCCAGCCTCTAGAACTGTAAGAAATAAATAT
TTGCTGTTTATAATCCAA

FIGURE 240

MGSSSFVLVLMVSLVLVTLVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC
YLHCGFKCVIPVKELEEGGNKDEDVSRPYPEPGWEAKCPGSSSTRCPQK

Signal sequence:

amino acids 1-19

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63

FIGURE 241

AAACCTCAGCACTTGCCGGAGTGGCTCATTGTTAAGACAAAGGGTGTGCACTTCTCGGCCAGG
 AAACCTGAGCGGTGAGACTCCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCC
 TCTAGAACCCGACCCACCACCA**ATG**AGGTCTCGCTGTGGAGATGCAGGACCTGAGCCAAGG
 CGTCCAGTGGTCTTGCTTCTGGCTGTCTGGTCTTCTTCTCTGCTGCGCTTGCCCTTTT
 TTAAGGAGCCTCAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAGAAAGGTCT
 CTACAGTCCCTGGCAAAGCCTAAGTCCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTA
 TGCAGAGCCAGCGCCAGAGAACATGCCCTCAACACACAAACCCAGGCCCAAGGCCACACCA
 CCGGAGACAGAGGAAAGGAGGCCAACCAGGCACCGCCGGAGGAGCAGGACAAGGTGCCCCAC
 ACAGCACAGAGGGCAGCATGGAAGAGCCACAGAAAAGAGAAAACCATGGTGAACACACTGTC
 ACCCAGAGGGCAAGATGCAGGGATGGCCCTCTGGCAGGACAGAGGCCAACAATCTGGAAGAGCC
 AGGACACAAAGACGACCCAAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACG
 GTGTGAGAGAAGCACCCAGGGCAAGCGGCAACCCACAGCCAAGACGCTCATTCCTCCAAAGTCA
 GCACAGAATGCTGGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCA
 CAGCAGTCATCCCACCTAAGGAGAAGAAACCTCAGGCCACCCACCCCTGCCCCCTTCCAG
 AGCCCCACGACGACAGAGAAACCAAGACTGAAGGCCGCCAACTTCAAATCTGAGCCTCGGTG
 GGATTTTGAGGAAAAATACAGCTTTCGAAATAGGAGGCCCTTCAGACGACTTGCCTGACTCTG
 TGAAGATCAAAGCCTCCAAGTCGCTGTGGCTCCAGAACTCTTTGCCCCAACCTCACTCTC
 TTCTGGACTCCAGACACTTCAACCAGAGTGAGTGGGACCGCCTGGAACACTTTGACCAACC
 CTTTGGCTTCATGGAGCTCAACTACTCCTTGGTGCAGAGGTCTGACACGCTTCCCTCCAG
 TGCCCCAGCAGCAGCTGCTCCTGGCCAGCCTCCCGCTGGGAGCCTCCGGTGCACTACCTGT
 GCCGTGGTGGGCAACGGGGGCATCTGAACAACTCCACATGGGCCAGGAGATAGACAGTCA
 CGACTACCTGTTCCGATTGAGCGGAGCTCTCATTAAGGCTACGAACAGGATGTGGGGACTC
 GGACATCCTCTACCGCTTTACCGCTTCTCCCTGACCCAGTCACTCCTTATATTGGGCAAT
 CGGGGTTTCAAGAACGTGCCTCTTGGGAAGGACGTCCGCTACTTGCACCTTCTGGAAGGCAC
 CCGGGACTATGAGTGGCTGGAAGCACTGCTTATGAATCAGACGGTGATGTCAA AAAACCTTT
 TCTGGTTCAAGCACAGACCCAGGAAGCTTTTCGGGAAGCCTGCACATGGACAGGTACCTG
 TTGCTGCACCCAGACTTTCTCCGATACATGAAGAACAGGTTTCTGAGGTCTAAGACCCCTGGA
 TGGTGCCCACTGGAGGATATACCGCCCCACCACTGGGGCCCTCCTGCTGCTCACTGCCCTTC
 AGCTCTGTGACCAAGGTGAGTGCTTATGGCTTCATCACTGAGGGCCATGAGCGCTTTTCTGAT
 CACTACTATGATACATCATGGAAGCGGCTGATCTTTTACATAAACCATGACTTCAAGCTGGA
 GAGAGAAGTCTGGAAGCGGCTACACGATGAAGGGATAATCCGGCTGTACACAGCGTCTGTGTC
 CCGGAACCTGCCAAAGCCAAAGAACT**TGA**CAGGGGCCAGGGCTGCCATGGTCTCCTTGCTGCTC
 CAAGGCACAGGATCAGTGGGAATCTTGAGACTTTTGCCATGCTCCAGGTGAGACTAA
 GCTCCAAGCCCTTCAGGAGTTCCAAGGGAACACTTGAACCATGGACAAGACTCTCTCAAGAT
 GGCAATGGCTAATTGAGGTTCTGAAGTTCTTCAGTACATTGCTGTAGTCTCTGAGGCCAGG
 GATTTTTAAATTAATGGGGTGATGGGTGGCCAAATACCAATTCCTGCTGAAAAACACTCTT
 CCAGTCCAAAAGCTTCTTGATACAGAAAAAGAGCCTGGATTTACAGAAACATATAGATCTG
 GTTGAATTCAGATCGAGTTTACAGTTGTGAAATCTTGAAGGTATTACTTAACTCACTAC
 AGATTGTCTAGAAGACCTTTCTAGGAGTTATCTGATCTAGAAGGGCTATACTTGTCTTGT
 TCTTTAAGCTATTTGACAACCTCTACGTGTGTGAGAAACTGATAATAATACAATGATTGT
 GTCCATGGAAAGGCAATAAATTTTCTACAGTGA AAAAAAAAAAAAAA

FIGURE 242

MRSCLWRCRHLSQGVQWSLLLAFLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLQSLAKP
KSQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAW
KSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTQGNNGGQTRKLTASRTVSEKHQ
KAATTAKTLIPKSQHRMLAPTGAIVSTRTRQKGVTAVIPPEKPKQATPPPAPFQSPTQRN
QRLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKFLPNLTLFLDSRHF
NQSEWDRLEHFAPPFGFMELNYSLVQKVVTRFPPVPPQQQLLASLPAGSLRCITCAVVGNGG
ILNNSHMQEIDSHDYVFRSLGALIKGYEQDVGTRTSFYGFATFSLTQSLLLILGNRGFKNVP
LGKDVRYLHFLEGTRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFFREALHMDRYLLHLPDFL
RYMKNRFLRSKTLGDAHWRIRPTTGALLLLTALQLCDQVSAYGFITEGHERFSDHYDTSW
KRLIFYINHDFKLEREVWKRLHDEGIIRLYQRP GGTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Lumenal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

CGATGCGCGGACCCGGGCACCCCTCTCTCTGGGGCTGCTGCTGGTGCTGGGGCCTTCGCCG
GAGCAGCGAGTGGAAATTGTTCCTCGAGATCTGAGGATGAAGACAAGTTTCTAAACACCT
TACAGGCCCTCTTTATTTAGTCAAAGTGCAGCAAACTTCCATAGACTTTATCAACA
CCAGAGACTGCACCATTCCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT
GTCAGTCCAGTGTGCATGGAGGATAAGTGAAGCAGACCGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCCCTGGAAACCAAGGGGAAACGAACTATCTTTATACACATCCCCCTATGG
ACAAGAGATTTATTTTGCAGACAGACTCTTCATAAGTCTTTGAGTTTGTATGTTGTTG
ACAGTTTGACAGATATATTCCGATAATCAGTGTACTTGCAGAGTGTTATCTGTCACCTATTT

[illegible]

MRGPGHPLLLGLLVLGPSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNT
RDCTIPAYYKRCARLLTRLAVSPVCMEDK

FIGURE 245

GGGCTGGGCCCCGCGCAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGAGG
CCCCACCCCGGCCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCCGCGCCG
CTCACCGCAATCGTCTGTGGTGCTGGGGGCTCCCCTGGTGCTGGCCGGCGAGGACTGCCT
GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTAACTGCGAGTTCTTCACCTTCT
GCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATCACCGAGAGG
CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT
CCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTCTGTTGCTACCTGT
ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTGTAAGGCCAGGAGATTCCAATGACAGGCATC
CCAGTGCAGCCAGTATACCCATACCCCGAGGACCCAAAGCTGGCCCTGCACCCCCACAGCC
TGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCAATATCCACTCTACCCAGCTGGGCCCC
CAGTCTACAACCCTGCAGTCTCTCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC
TGAGGAACCAGCCATGTCTCTGCTGCCCCTTCACTGATGCCAACCTTGGGAGATGCCTCAT
CCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGTCTCCAGCCACCAGGCCCCAGACCAA
GCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGAACAGGAGCTGAACTAGA
ACTATGAGGGGTGGGGGGAGGGCTTGAATTATGGGCTATTTTACTGGGGGCAAGGGAGG
GAGATGACAGCCTGGGTACAGTGCCTGTTTTCAAATAGTCCCTCTGCTCCCAGATCCCAG
CCAGGAAGGCTGGGGCCCTACTGTTTGTCCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGT
TCCGTCAGCAGCTGGCAGTAGCCCTCCTCTCTGGCTGCCCACTGGCCACATCTCTGGCCTG
CTAGATTAAAGCTGTAAAGACAAAA

FIGURE 246

MPPAGLRRAAPLTAIALLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHRYC
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQLQSP
FEGQEIPMTGIPVQFVYPYPQDFKAGFAPPQPGFMYPPSGFAPQYPLYPAGPPVYNPAAPP
YMPPQPSYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

FIGURE 247

FIGURE 248

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVH
YDLLIHANLTLTLFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPLOVLE
HPPEQEQIALLAPEPLLVGLPYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA
ARMAFPCFDEPAFKASFSIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMMSTYLV
FIISDFESVSKITKSGVKVSVYAVPDKINQADYALDAAVTLLFEFYEDYFSIPYPLPKQDLAA
IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHELAHQWFGNLVTMEWWNDL
WLNEGFAKFMFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD
DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMACICPTDGVKGM
FCSRSQHSSSSSHHQEGVDVKTMMNTWTLQRGFPLITITVRGRNVHMKQEHYMKSGDGAPD
TGYLWHVPLTFITSKSNMVHRFLKTKTDVLILPEEVEWIKFNVGMNGYIIVHYEDDGWDSL
TGLLKGTHTAVSSNDRASLINNAFQLVSIKLSIEKALDLSLYLKHETEIMPVFQGLNELIP
MYKLMEKRDMMNEVETQFKAFLIRLLRLDIDKQTTWDEGSVSEQMLRSELALLACVHNYYQPCV
QRAEGYFRKWKESNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSTEKSQIEFALC
RTQNKELQLWLLDESFKGDKIKTQEFFQILTLIGRNPVGYPLAWQFLRKNWNKLQKFELGS
SSIAHVMVGTNTQFSTRRLLEEVEKGGFFSSLKENGSQLRCVQQTITETIENIGWMDKNFDKIR
VWLQSEKLERM

Signal peptide:

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metallopeptidases, zinc-binding region signature:

amino acids 350-360

FIGURE 249

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCAC
TGCCAGGAGTGACGGCGTGCCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGCC
GACCTACCCCGGCAATGGACCCTAAGAACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA
CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCAAGGGCTGCACGG
AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC
TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG
AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACTGTTATGAT
GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGA
ACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGACCACCATTATGACACACGAAAC
TTGGCTCAAGAACCACCTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT
GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCTGGTGGGGACAAAAG
GCTGCAGCACTGTTGGGGCTCAAAATTCCAGAAGACCACCATCCACTCAGCCCCCTCCTGGG
GTGCTTGTGGCCTCCTATACCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
CAGCGTTCTGCTGAACCTCCCTCCCTCCTCAAGCTGCCCTGTGCCAGGAGACCGGCAGTGTC
CTACCTGTGTGCAGCCCCCTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
GGCGCCACTCATTGTTATGATGGGTACATTCACTCTCAGGAGGTGGCGTGTCACCAAAAAT
GAGCATTCAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTGAACCACACCAGACAAATCG
GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG
GTGGGGAGTGGTTTGCCCTTCTGCTTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGA
CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGACACCAGATTCTTTC
CCATTCTGTCCATGAATCATCTTCCCACACACAATCATTATCTACTACCTAACAGCA
ACACTGGGGAGAGCCTGGAGCATCCGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTG
GCTGCATGTATCTGATAATACAGACCTGTCCTTTCA

FIGURE 250

MSAVILLALLGFILPLPGVQALLCQFGTVQHVKVSDLPQWTPKNTSCDSGLGCQDTLMLI
ESGFPQVSLVLSKGCTEAKDQEPRVTEHRMGFGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTHCYDGLRLRGGGIFSNLRVQGCMPQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVC
PSC

FIGURE 251

GCGACGGGCAGGACGCCCGTTGCGCTAGCGCGTGCTCAGGAGTTGGTGTCTGCGCTGCGCT
CAGGATGAGGGGGAATCTGCGCCTGGTGGCGGTTCTAATCAGCCCTGGCCTTCTGTCTGCTGCTG
CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTCGTCCCTGG
CCTCAAAGGGGATCGGGAGAGAAGGGAGACAAAGGCGCCCCGACGGCCTGGAAGAGTCG
GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTGCTCAT
GGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC
TGGTCTTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG
AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTGCGC
GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA
CGCCACAGCTGTCTGCCAGGGCCGCGGGGGCACGCTGAGCATGCCCAAGGACAGGGCTGCCA
ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTGGCCCGTGTCTTCATCGGCATCAAC
GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCATGCGGACCTTCAACAA
GTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGGACTGCGTGAGATGGTGGCCT
CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAAG
GAGAACATGTGAGCCTCAGGCTGGGGCTGCCCATTTGGGGGGCCCCACATGTCCCTGCAGGGTT
GGCAGGGACAGAGCCCAGACCATGGTGCCAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAG
GCTCACTGAGTAGAGGGCTGTTGTCTAAACTGAGAAAAAGGCCCTATGCTTAAGAGGAAAATG
AAAGTGTTCTGGGGTGCTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA
ATGTCAATTATGTAATTATTACCCAGAATTGCTCTTCCATAAAGCTGTGCCTTTGTCCAAGC
TATACAATAAAATCTTTAAGTAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAAA

MRGNLALVGLISLAFSLPSGHQPAGDDACSVQILVPLKGDAGEKGDKGAPGRPRGVG
PTGEKGMGMDKGQKGSVGRHGKIGPIGSKGEKSGDGTGPPGPNGEPLGPCESQLRKATIGE
MDNQVSQLTSELKFIKNVAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGTLSPMKDEAAN
GLMAAYLAQAGLARVFCEINDLEKEGAFVYSDHSPMRTFNKWSRGEPNNAYDEEDCVEMVAS
GGMNDVACHTTMYTFIGEDDKENM

FIGURE 253

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG
CACCAGTGTGTGAGGGGAGCAGGCAGCGGTCCTAGCCAGTTCTTGATCCTGCCAGACCACC
CAGCCCCCGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGTGCTATTTCACAGCCAT
CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG
TTCTTGCGGGGGGCCGAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC
AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA
GGAATCAACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA
GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCCTCGGCCC
CTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCTGGGAACAGAGGAGCAGAGACC
TTTTAAGACTCTCCTACGGATGTGAATCAAGAGAACGTCCCAGCTTTGGCATCTCAAGT
ATCCCCCGAGAGCAGAATAGGTACTCCACTTCGGGACTCCTGGACTGCATTAGGAAGACCTC
TTTCCCTGTCCCAATCCCAGGTGCGCACGCTCCTGTTACCTTTCTCTCCCTGTTCTTGT
AACATTCTTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCTGGTGTGGAAACTGCA
TAGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCTCTGTAGTGT
CCTACATTAAAAATATAATGTCTCTCTATTCTCAACAATAAAGGATTTTTCATATGAA
AA

FIGURE 254

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPEKRDMDFFVGLMGKRSVQPEGKTGPFLPSVRVPRPLHPNQLGSTGK
SSLGTEEQRPPL

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

FIGURE 255

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCGCTGTGCCCTGCTGTGCC
 CGCGCTGTCCGCCGTGCTACCGCTCTGCTGGACGCGGAGAGCCAGCGAGCTGGTGATTG
 GAGCCCTGCGGAGAGCTCAAGCGCCAGCTCTGCCCCAGGAGCCAGGCTGCCCCGTGAGTC
 CCATAGTTGCTGCAGGAGTGGAGCCATGAGCTGCGTCTCGGGTGGTGTATCCCCCTGGGGC
 TGCTGTTCTGGTCTGCGGATCCCAAGGCTACCTCCTGCCCA^ΔCGTCACTCTCTAGAGGAG
 CTGCTCAGCAAATACCAGCACAACGAGTCTCACTCCCGGGTCCGCAGAGCCATCCCCAGGGA
 GGACAAGGAGGAGATCCTCATGTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCCT
 CCAACATGGAGTACATGGTGAGCGCCGGCTCCGGCCGAGAGGCTGGCACCGGGGGTGGGGC
 CTGGGCCACAGCCTGCTCTGTTCCCCAGCCAGCTCTGTTCCCCAGCCAGTGCCTGTGATGG
 CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTTGTTGTTGTT
 TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGAATGGACAATCGTCATGCCCTG
 AAACCTTAGACTCCCAGGGTTAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACTACAG
 GCATGCACCATGGTGCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGTCTTGCTACGT
 TGCCAGGCTGGTCTTGAACCTCCTAGGCTCAAGCAATCCTCCTGCCTCAGCCTCTCAAAGTG
 CTAGGATTATAGGCATGAGTACCCCTGTCTGGCTCTGGCTCTGTTCTTAACATTCTGCCAAA
 ACAACACACGTGGGTTCCTGTGCAGAGCCTGCCTCGTTGCCTTCATGTCACTCTTGGTAGC
 TCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGAGGGGGCCAGGG
 CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACAGCTAGCTGCACCACCCTGACTTCTC
 CTTAGCCCGTGTGAGCCTCACTTTCACCTTGGAGAGTCCCTCCTCGCGTGGTTGCCATGACT
 GTGAGATAAGTCGAGGCTGTGAAGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGG
 CTTTGCTAACCAGGAAAGGAGCTAACGGTGACAGAAGACAGCCAAGGTCAACCTCCTCGGGT
 GATTGTGATGGGTGTTCCAGGTGTGGTTGGGCGATGCTGCTACTTGACCCCAAGCTCCAGTG
 TGGAAACTCCTTCTCGGCTGGTTTTCCAGAACTACAGAGGAATGGACCACAGTCTTCCAGG
 GTCCTCCTCGTCCACCAACCGGAGCCTCCACCTTGCCATCCGTGAGCTATGAATGGCTT
 TTTAAACAAACCCAGCTCCAGCCTGGGTAACATGGTAAAGCCCCGTCTCTACAAAAAATC
 CAAGTTAGCCGGGCATGGTGGTGCACCTGTAGTCCCAGCTGCAGTGGGACTGAGGTGGAG
 GTGGAGGTGGGGGGTGGGAGCTGAGGAAGGAGGATCGCTTGAGCCTGGGAAGTCGAGGCTGC
 AGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGCCCTGTCTCAAAAA

256/330

FIGURE 256

MSCVLGGV IPLGLFLVCGSQGYLLPNVTLLLEELLSKYQHNEHSRVRRAIPREDKEEILML
HNKLRGQVQPQASNMEYMSVAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGWLRVSSGR
GGSRLCSVLFVCFETGSHSATDAGVQWHNRHALKP

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

FIGURE 257

AAGGAGAGGCCACCGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACT**ATG**GG
GTCTGGGCTGCCCCCTTGTCCTCCTCTTGACCCCTCCTTGGCAGCTCACATGGAACAGGGCCGG
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGC
TTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA**TGA**CAGCCATTGAAGCCTG
TGTCTTCTTGGCCCGGGCTTTTGGCCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTT
CAGCAGGCCCCACCCTCCTGAGTGGCAATAAATAAAATTCGGTATGCTG

258/330

FIGURE 258

MGSGLPVLVLLTLLGSSHGTGPGMTLQLKLESFLTNSSYESSFLELLEKLCLLLHLPSTGTS
VTLHHARSQHHVVCNT

100
90
80
70
60
50
40
30
20
10
0
100
90
80
70
60
50
40
30
20
10
0

FIGURE 259

AATTGTATCTGTGTAATGTTAAAACAAACGAAATAAAATAGAAGGAAAAACTTTCTGAGTTT
CAAAAACAACAGACTAGTACTCTAAAGAAGCTCTTTAAACAATTAAGTGTAGGATTGCAGT
TATGATTGGATATTATTTAATTCTGTTTCTGATGTGGGGTTCTCCACTGTGTTCTGTGTGC
TATTAAATATTTACCATTCGAGAAGCTTCATTCAGTGTTGAAATGAATGCTTAGTGGATCTG
TGCCTCTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTTCCCTCCC
CTCCGATTGTTCTAAA**TAA**TTGAAAGATGTCTGCTGTGGAAAAGGCATGTATTAAATCTG
TATGATTCTCAACCATCTTTAGTTGGGAAAGGTCCTTGAAAGCCAATGGAATACTTTTTTT
TTTTCTTGGCACTAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTA
GTAAATAGAAACCTGTGTTTATTCTCAGGTATTTAGAAACAACAGCCATCATTTTATTTT
ATGTGTGTGTTCTTGGCTGTATTCATAAATTATATATTTTGGGCTATCAAATATTACTTCAT
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTTCTAGTGCATTTTCTC
AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTA
TCTTCAGATTACTTGATTCAAATAAACCAATTATGTTTGAATTGATATTAATAAAACCAGA
ATAAAAGTTCATATCTACCC

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FIGURE 260

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECVLVDLCLLRICYKLSGVPNQCRVPLP
SDCSK

Important features:

Signal peptide:

amino acids 1-29

FIGURE 261

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGACCACCGGAGCCCTTGAGACATCCTT
 GAGAAGAGCCACAGCATAGAGACTGCCTTCTGGTGTTTTGCAGC**ATGAT**GGTGGCCCTT
 CGAGGAGCTTCTGCATTGCTGGTCTGTTCCTTGCAGCTTTTCTGCCCCCGCCCGAGTGAC
 CCAGGACCCAGCCATGGTGCATTACATCTACCAGCGCTTTCGAGTCTTGGAGCAAGGGCTGG
 AAAAATGTACCCAAGCAACGAGGGCATACATTTCAAGAATTCGAAGAGTTCTCAAAAAATATA
 TCTGTCTATGCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAGAGTGCAGTGGGTAACTT
 GGCAGTGAAGTGTGAACGTGCCAACGGGAGATTGACTACATACAATACCTTCGAGAGGCTG
 ACGAGTGCATCCTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAA
 GAGAAAAAGATCCGGAAGTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTC
 TTTGAAAATAGTGAAGAAGATGATGGACACACATGGCTCTGGATGAAAGATGCTGCTATA
 ACTCTCCAAGGTGTAAGTATTAAATTGGATCCAGAAACAACACTGTTGGGAATTTGCAAAAC
 ATACGGGCATTCATGGAGGATAACACCAAGCCAGCTCCCCGGAAGCAAAATCCTAACACTTTC
 CTGGCAGGGAACAGGCCAAGTGATCTACAAGGTTTTCTATTTTTTCATAACCAAGCAACTT
 CTAATGAGATAATCAAAATAAACCTGCAGAAGAGGACTGTGGAAGATCGAATGCTGCTCCCA
 GGAGGGGTAGGCCGAGCATTGGTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGT
 GGATGAGCATGGGCTCTGGGCCATCCACTCTGGGCCAGGCACCCATAGCCATTGTTGTTCTCA
 CAAAGATTGAGCCGGGCACACTGGGAGTGGAGCATTCATGGGATACCCCATGCGAGAAGCCAG
 GATGCTGAAGCCTCATTCCTCTTGTGTGGGGTCTCTATGTGGTCTACAGTACTGGGGGCCA
 GGGCCCTCATCCGATCCGATCTATGATCCACTGGGCACTATCAGTGAGGAGGACTTGC
 CCAACTTGTCTCTCCCAAGAGACCCAGAAGTCACTCCATGATCCATTACAACCCCAAGAGAT
 AAGCAGCTCTATGCTTGAATGAAGGAAACAGATCATTTACAAACTCCAGACAAAGAGAGAA
 GCTGCCCTCTGAAG**TAA**TGCAATTACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTTT
 TACAGGACAGTGAGGCTATAGCCCTTACAAATATAGTATCCCTCTAATCACACACAGGAAG
 AGTGTGTAGAAGTGAATAACGTATGCTCTTTCCCAAATGTCACTGCCTTAGGTATCTTC
 CAAGAGCTTAGATGAGGACATATCATCAGGAAGTTTCAACATGTCATTACTCCCCCAA
 CCTCTGGCTCTCAAGGATGACCACATTCGTATACAGCCTACTTCAAGCCTTTTGTGTTTACT
 GCTCCCCAGCATTTACTGTAACCTCTGCCATCTCCCTCCCAATTAGAGTTGTATGCCAGC
 CCCTAATATTCACCACTGGCTTTTCTCTCCCTGGCCCTTGTCTGAAGCTCTTCCCTCTTTT
 CAAATGTCTATTGATATTTCTCCATTTTCACTGCCCAACTAAAATATCTATTAATATTTCTTT
 CTTTCTTTTCTTTTGTGAGACAAGGTCTCACTATGTTGCCAGGCTGGTCTCAAACTCC
 AGAGCTCAAGAGATCTCTGCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCAC
 CACACCTGGCTTAAAAATCTATTCTTATTGAGTTTAACTCTATTTCCTTCCCTAGCCCTGTC
 CTTCCCACTAAGCTTGGTAGATGTAATAATAAAGTGAAAATATTAACATTGAAATATCGCTTT
 CCAGGTGTGGAGTGTGTGCACATCATTGAATTCTCGTTTCACTTTGTGAAACATGCACAAG
 TCTTTACAGCTGTCTATTCTAGAGTTTAGTGGAGTGAACAAATACAAAGTGAAGATACAGC
 TAGAAAATACATAAATCCCATAGTTTTTCCATTGCCCAAGGAAGCATCAAAATACGTATGTT
 TGTTCACCTACTCTTATAGTCAATGCGTTCATCGTTTCAGCCTAAAAATATAGTCTGTGCC
 TTTAGCCAGTTTTCATGTCTGCACAAGACCTTTCAATAGGCCCTTCAAAATGATAAATTCCTCC
 AGAAAAACAGTCTAAGGGTGAAGACCCCACTCTAGCCTCCCTTGTCTTGTCTGCTCTGCTCTGT
 TTCTCTCTTTCTGCTTTAAATTCAATAAAAGTGACACTGAGCAAAAAA

FIGURE 262

MMVALRGASALLVLFLLAFLPPPQCTQDPAMVHYIYQRFVRVLEQGLEKCTQATRAYIQEFQE
FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQRIDYIQYLREADECIVSEDKTLAEMLL
QEAEKEKKIRTLNLNASCNDMLMGIKSLKIVKMMMDTHGSWMKDAVYNSPKVYLLIGSRNNTV
WEFANIRAFMEDNTKPAPRKQILTLWQGTGQVIYKGFLFFHNQATSNEIIKYNLQKRTVED
RMLLPGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEPPTLGVEHSWDT
PCRSQDAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFPPKRPRSHSMIH
YNPRDKQLYAWNENQIIYKLQTKRKLPLK

FIGURE 264

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPPDKSSGSKKQK
QYQIRKEKPQQHNFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ
REHRSMRANVELDHATLVRFSPDCRAFIVWLANGDTLRVFKMTKREDGGYTFTATPEDFPPK
HKAPVIDIGIANTGKFIMTASSDTTVLIWLSLKGQVLSTINTNQMNTHAAVSPCGRFVASC
FTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV
EYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHILKRASNESTRQLQQQLTQ
AQETLKS LGALKK

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 265

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG
CAGTGTTTTGCCTTCACCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGCTCC
TCCTAGTAACCTGTGTCTGACTGTGCTGTGATCACAGGGCCTGTGAGCGGGATGTCCAGTGT
GGGGCAGGCACCTGTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCACCCCGCT
GGGGCGGGAAGGCGAGGAGTGCCACCCCGGCAGGCACAAGGTCCTTCTCTCAGGAAACGCA
AGCACCACACCTGTCTTGCTTGCCCAACCTGTGTGTCTCCAGGTTCCCGGACGGCAGGTAC
CGCTGTCTCCATGGACTTGAAGAACATCAATTTTTAGGGCGCTTGCTGGTCTCAGGATACCCA
CCATCCTTTTCTGAGCACAGCCTGGATTTTATTCTGCCATGAAACCCAGCTCCCATGAC
TCTCCAGTCCCTACACTGACTACCCTGATCTCTCTTGTCTAGTACGCACATATGCACACAG
GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTCACAGCTTGAGG
CTGTGGTGTGAAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTA
AATGGCAGAAAGGACATTCCCCCTCCCCCTCCCCAGGTGACCTGCTCTCTTCCCTGGGCCCTG
CCCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCTGGGCACAGGCTCTTGGGT
GCATTGCTCAGAGTCCCAGGTCTGGCCTGACCTCAGGCCCTTACCGTGAAGTCTGTGAGG
ACCAATTTGTGGGTAGTTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGAC
TCAAGATTGGCTCTTCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCA
GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTTGTGGCCTGTGA
CCTGTGACCTTCTGCCAGAATTGTCATGCCTCTGAGGCCCTCTTACCACACTTTACCAGT
TAACCACTGAAGCCCCCAATTCCACAGCTTTTCCATTAAATGCAATGGTGGTGGTTCAA
TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTTCCTTAAACAACCTCTTTCCA
AGGATCAGCCCTGAGAGCAGGTTGGTGACTTTGAGGAGGGCAGTCTCTGTCCAGATTGGGG
TGGGAGCAAGGGACAGGGAGCAGGGCAGGGGCTGAAAGGGGCAGTGATTGAGACCAGGGAGG
CAACTACACACCAACATGCTGGCTTTAGAATAAAAGCACCAACTGAAAAA

266/330

FIGURE 266

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGECHP
GSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSDMLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

FIGURE 267

AGCGCCCCGGCGTCGGGGCGGTAAAAGCCGCGCAGAAGGGAGGCACCTTGAGAAATGTCTTTTC
 CTCAGGACCCCAAGTTTCTTCACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGC
 TGCTGCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGG
 CCCTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAAA
 GCAAAGGAGCTATGGGAAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTT
 CCTCTGTCGAGAGGAAGCTGCGGATCTGTCTCCCTGAAAAGCATGTTGGACCAGCTGGGCG
 TCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCAGCCTTAT
 TTCAAAGGAGAAATCTTCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGGCGGAAGAT
 GATGTTTATGGGATTTATCCGCTCTGGGAGTGTGGTACAACCTTCTCCGAGCCTGGAACGGAG
 GCTTCTCTGGAACCTTGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTCGTGGTGGGATCA
 GGAAGCAGGGCATTCTTCTTGAGCACCAGAAAAAGAATTTGGAGACAAAGTAAACCTACT
 TTCTGTTCTGGAAGCTGCTAAGATGATCAAACCACAGACTTTGGCCTCAGAGAAAAAATGAT
 TGTGTGAAACTGCCAGCTCAGGGATAACCAGGGACATTCACCTGTGTTTATGGGATGTATT
 GTTTCCACTCGTGTCCCTAAGGAGTGAGAAACCCATTTATACTCTACTCTCAGTATGGATTA
 TTAATGTATTTTAATATTCTGTTTAGGCCCACTAAGGCAAAATAGCCCCAAAACAAGACTGA
 CAAAAATCTGAAAACTAATGAGGATTATTAAGCTAAACCTGGGAAATAGGAGGCTTAAAA
 TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCAGCAGCTTTGGGAGGCCAAGG
 TGAGCAAGTCACCTTGAGGTCGGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTC
 TCTACTAAAAATACAAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCAGCTACCCG
 GGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTCGCGTGAGCTGAGATCA
 CACCAGTGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

FIGURE 268

MSFLQDPSFTFMGMWSIGAGALGAALALLLANTDVFLSKPQKALEYLEDIDLKLEKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSLMDQLGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKKFYGPQRKMMFMGFIRLGVVYNFFRAWNGGFSGNLEGEFILGGVFV
VGSGKQGILLEHREKEFGDKVNLVSVLEAAKMIKPOTLASEKK

FIGURE 269

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCG
GGCCAGGTGCCCCGTGCGAGGTGCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGA
AGCCCCCTCCTCGGCGCTGCCAACCCGCCACCCAGCCCATGGCGAACCCTGGGGCTGGGGCTG
CTTCTGGCGCTGGGCCTGCCGTTCTGCTGCCCCGCTGGGGCCGAGCCTGGGGGCAAATACA
GACCACTTCTGCAAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATG
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTGGCTGCCTTG
CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG
CACCTACCGGCCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG
ACTCCAAGGAGACGGTGCAGGGCTGCCTGCCCATCTAGGTCCCCCTCTCCTGCATCTGTCTCC
CTTCATTGCTGTGTGACCTTGGGGAAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG
TGCTTAATAGCAGGAAGAAGGTACTTCAAAGACTCTGCCCTGAGGTCAAAGAGAGGATGGG
GCTATTCACTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

270/330

FIGURE 270

MANPGLGLLLALGLPFLRLRWGRAWGQIQTTSANENSTVLPSTSSSSDGNLRPEAITAIIV
VFSLLAALLLAVGLALLVRKLEKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

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FIGURE 271

AATATATCATCTATTTATCATTAAATCAATAATGTATTCTTTTATTCCAATAACATTTGGGTT
TTGGGATTTTAAATTTTCAAACACAGCAGAAATGACATTTTCTGTCACTATTATTATTGTTG
GTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCT
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA
GGGTAAATCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATG
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATA
TATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT
TTATTAATTTTAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTTGATACAATAAAAGAAAAGTGTCTCTCCCTTACAGAATTGACATTTTAA
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAGGAA
AGAAGGGAAAATGTTGCCAAGGAAAAAAAAA

272/330

FIGURE 272

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK
GIVKGRNLDSRGLILGAEAWGRGVKKNT

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FIGURE 273

GCCAGGAATAACTAGAGAGGAACA**ATG**GGGTTATTAGAGGTTTGTGTTTCCCTCTTAGTTCT
 GTGCCCTGTCACCAAGCTCAAATACTTCCTTCATTAAGCTGAATAAATAGGCTTTGAAGATA
 TTGTCATTGTTATAGATCTTAGTGTGCCAGAAGTAAAAAATAATTGAACAAATAGAGAT
 ATGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAGATTTTTTTCAGAAA
 TGTATCTATATTAATTCCTGAGAATTGGAAGGAAAATCCTCAGTACAAAGGCCAAACATG
 AAAACCATAAACATCTGTAGTTATAGTTGCACACCTACACTCCGAGGTAGACATGAACCT
 TACACCAGAGCTTCAGAGATGTGGAGAGAAAGCGAATACATTCACCTCACCCCTGACCT
 TCTACTTGGAAAAAACAATAATGAATATGGACACCAGGCAAACTGTTGTCCATGAGTGGG
 CTCACCTCCGGTGGGGAGTGTGTTGATGAGTACAATGAAGATCAGCCTTCTCATCGGTCAAG
 TCAAAAAAATCGAAGCAACAAGGTGTTCCCGAGGTATCTCTGGTAGAAATAGAGTTTATAA
 GTGTCAAGGAGGCACTGCTTTAGTAGAGCATGCAGAATTGATTTCTACAAACAAATCTGATG
 GAAAAGATTGTCAATCTTCTCTGATAAAGTACAAACAGAAAAGCATCCATAATGTTTATG
 CAAAGTATTGATTTCTGTTGTTGAATTTTGTAAACGAAAAAACCATAACTCAAGAGCTCCAAG
 CCTACAAAAACATAAAGTGAATTTTAGAAGTACATGGGAGGTGATTAGCAATCTGAGGATT
 TTA AAAACACCATACCCATGGTGACACCACTCTCCACCTGCTCTCTCATTTGCTGAAGATC
 AGTCAAAAGAAATGTGTGCTTAGTCTTGATAAGTCTGGAAGCATGGGGGTAGGACCGCCT
 AAATCGAATGAATCAAGCAGCAAAAACATTTCTGCTGAGCATTAATGAAAATGGATCTGGG
 TGGGGATGGTTACATTTGATAGTACTGCCACTATTGTAATTAAGCTTAATCCAAATAAAAAAG
 AGTGTGAAGAAACACACTCATGGCAGGATTACCTACATATCTCTGGGAGGAACCTTCCAT
 CTGCTCTGGAATTAATATGCAATTCAGGTGATTGGAGAGCTACATTTCCCAACTCGATGGAT
 CCGAAGTACTGCTGCTGACTGATGGGGAGGATAACACTGCAAGTCTTCTGATTGATGAAGT
 AAACAAAGTGGGGCCATTTCTCAATTTATTGCTTTGGGAAGAGCTGCTGATGAAGCAGTAAT
 AGAGATGAGCAGGATAACAGGAGGAAGTCAATTTTATTTTTCAGATGAAGCTCAGAACAAATG
 GCCTCATTGATGCTTTTGGGGCTCTTACATCAGGAAATCTGATCTCTCCAGAGAGTCCCTT
 GAGCTCGAAAGTAGAGGGATTAACTGGAACATAATGGAATACTCTCGAGCAGCAATTTCTGTGC
 CTCCAATCAGAGTGAATGCTAAATGAATAAGGACGTAACAGTTTCCCGACGCCAATGATT
 GTTTACGCAAAAATTTCAAGGATATGTACCTGTCTTGGAGCCAAATGTGACTGCTTTTCAT
 TGAATCAGAGAAATGGACATACAGAAGTTTGGAACTTTTGGATAATGGTGCAGGCGCTGATT
 CTTTCAAGAAATGATGGAGTCTACTCCAGGTATTTACAGCATATACAGAAAATGGCAGATAT
 AGCTTAAAAGTTCGGGCTCATGGAGGAGCAAACTGCCAGGCTAAAATATCGCGCTTCCACT
 GAATAGAGCCGCGTACATACAGGCTGGGTAGTGAACGGGGAAATGAAGCAAAACCGCCAA
 GACCTGAATTTGATGAGGATACCTCAGACCACCTTGGAGGATTTACGCCGAACAGCATCCCGGA
 GGTGTCATTTGGGTATCACAAGTCCCAAGCCTTCCCTTGCCGTGACCAATACCCACAGTCA
 AATCAGAGACCTTGATGCCACAGTTTATGAGGATAAGATTTATCTTACATGGACAGCAGCAG
 GAGATAATTTTGTGTTGGAAAAGTTCAACGTTATATCATAGAATAAGTGCAAGTATTCTTT
 GATCTAAGAGACAGTTTTGATGATGCTCTTCAAGTAATACTACTGATCTGTCAACCAAGGA
 GGCCAGACTCCAAGGAAAGCTTTGCATTTAAACCGAAAATATCTCAGAAGAAAATGCAACCC
 ACATATTTATGCCATTTAAAGTATAGATAAAAGCAATTTGACATCAAAGTATCCAACTT
 GCACAAGTAACCTTTGTTATCTCCCTCAAGCAATCTGTATGACATTGATCCTACCTACTCC
 TACTCCTACTCCTACTCCTGATAAAAGTCATAATTTCTGGAGTTAATATTTCTACGCTGGTAT
 TGCTGTGGTCTGTTGTAATTTGTTAACTTTATTTAAGTACCACCATTT**TGAA**CCCTTA
 ACGAAGAAAAAATCTCAAGTAGACCTAGAAGAGAGTTTTAAAAAACAAAAACAATGTAAGT
 AAAGATATTTCTGAATCTTAAATTCATCCCATGTGTGATCATAAACTCATAAAAATAATT
 TTAAGATGTCGGAAAAAGGATCTTTGATTAATAAAAAACATCATGGAATATGTA AAAACCTGT
 CAAGATTAATAATTTAATAGTTTCATTTATTTGTTATTTGTAAGAAATAGTGAATGAC
 AAAGATCCTTTTTCATACCTGATACCTGGTTGTATATTTATGATGCAACAGTTTTCTGAAAT
 GATATTTCAAATGTCATCAAGAAATTAATAATCATCTCTGATGATCAAATCAAGATAAA
 GGAGAGCAATAAACCAACATTTGGA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 274

MGLFRGFVFLVLVCLLHQSNSTSFIKLNNNGFEDIVIVIDPSVPEDEKIIIEQIEDMVTTASTY
 LFEATEKRFFFKNVSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTEC
 GEKGEYIHFTPDLLLGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPPYRAKSKKIEATR
 CSAGISGRNRVYKCGGSCLSRACRIDSTTKLYGKDCQFFPDVKQTEKASIMFMQSIDSVVE
 FCNEKTHNQEAPSLQNIKNFRSTWEVISNSEDFKNTIPMVTPPPPVFSLLKISQRIVCLV
 LDKSGSMGGKDRLNRMNQAAKHFLQTVENGSWGMVHFDSTATIVNKLIQIKSSDERNTLM
 AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLTDGEDNTASSCIDEVKQSGAIVH
 FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLT
 LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSTIMENFTVDATSKMAYLSIPG
 TAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKMNDVNSFPSPMIVYAEILQG
 YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNQGVYSRYFTAYTENGRYSLKVRAGH
 GANTARLKLRPPLNRAAYIPGWVNGEIEANPPREIDEDTQTTLDEFSRTASGGAFVVSQV
 PSLPLPDQYPPSQITDLDATVHEDKIIILTWTAPGDNFVGKQVRYIIRISASILDLRDSFDD
 ALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSNIAQVTLFIP
 QANPDDIDPTPTPTPTPKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.
 amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
 628-632, 811-815, 832-836, 837-841, 852-856, 896-900

[illegible]

FIGURE 276

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQALALPRANSPTGKEGYQAVLQ
EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFL
HSQVDKAEVNAGVKLATEYAAVFPDSFTLQKVYQLETGLTRHPPEKFPVRKDKRDELVEAIES
ALETLNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPI
MKVKNEKLNMAANTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCR
LNTQPGKKVFYPVLFSQYNPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI
NIGGFDLDIKGWGGEDVHLYRKYLSNLIVVRTPVRLFHLWHEKRCMDELTPEQYKCMQS
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT

FIGURE 277

GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACC
 AGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT
 ATGCCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA
 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCCTACTTTGCAATGTAACCCAGAGGGT
 ATCATTTCTGGTTTGTGGTTACAGACCCCTTCAAAAAATCACACCCCTTCCTGCTGTTGAGGTGC
 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACCT
 CTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTG
 GATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTAT
 CAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGAT
 AAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCTCTGATCCCCTGGACATGAAGGG
 GGGCATATTAAATGATGCCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT
 TGTCTGCTTCCTCAAGAAATTAACATTTGTTTCTGTGTACTGCTGAGCATCCTGAAATA
 CCAAGAGCAGATCATATATTTTGTTCACCATTTCTCTTTTGTAATAAAATTTTGAAATGTGCT
 TGAAAGTGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTACAGAC
 TCAAAATATTCTAAATATTTTTCTGACAGTATAGTGATAAAATGGTGCATGTGGTATTG
 TAGTTATTGATTTAAGCATTTTTAGAAATAAGATCAGGCATATGTATATATTTTACACTTC
 AAAGACCTAAGGAAAAATAAATTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT
 TGAAGATGGATCCTTTTTGACGATCACTTATATCACCTCTGTATATGACTAAGTAAACAAAAG
 TGAGAAGTAATTATTGTAATGGATGGATAAAAATGGAATTACTCATATACAGGGTGAATT
 TTATCTGTTATCACCAACAGTTGATTATATATTTTCTGAATATCAGCCCCATAAGGAC
 AATTCTATTGTTGACCATTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAG
 TAATAATCATCTCTTTTTAAAAA



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MLWLFFFLVTAIHAELCPQGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVP
NREATEISHVLLCNVTQRVSFWFVTDPSKNHTLPAVEVQSAIRMKNRINNAFFLNDQTL
FLKIPSTLAPMPDPSVPIWIIIFGVIFCIIIVAIALILSGIWQRRRNKEPSEVDDAEDKC
ENMITIENGIPSDPLDMKGGILMMP

FIGURE 279

AACTCAAACCTCCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGAGTGCCCTTGGCAGG
GTGTTTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTCATGT
ATGGCAAGAGCTCTACTCGTGCGGTGCTTCTTCTCCTTGGCATAACAGCTCACAGCTCTTTGG
CCTATAGCAGCTGTGGAAATTTATACCTCCCGGGTGCTGGAGGCTGTTAATGGGACAGATGC
TCGGTTAAAATGCACCTTTCTCCAGCTTTGCCCCCTGTGGGTGATGCTCTAACAGTGACCTGGA
ATTTTCGTCCTCTAGACGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC
CAACCCATGAGTGGGCGGTTTAAAGACCGGGTGCTTGGGATGGGAATCCTGAGCGGTACGA
TGCCTCCATCCTTCTCTGGAAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGA
AGAACCCACCTGATGTTGATGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA
CGCTTCTCTGAGATCCACTTCTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT
AATAGTAATTGTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC
ATAAAGTGGTGGAGATAAAATCAAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCCT
GTTTATTTAGAAGACACAGACTTAAACAATTTTAGATGGAAGCTGAGATGATTTCGAAGACAA
GAACCCTAGTATTTCTTGAAGTTAATGGAACCTTTCTTTTGCTTTTCCAGTTGTGACCCGT
TTTCCAACCAAGTTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC
AGTGCTCCTCCATATCACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTTCA
GTGTAATTTTTCAAGTGCTCATTAGGTTTTATAACAAGAAGCTACATTTTTTGCCCTTAA
GACACTACTTACAGTGTATGACTTGTATACACATATATTGGTATCAAAGGGGATAAAAGCC
AATTGTCTGTACATTTCCCTTCACGTATTTCTTTAGCAGCACTTCTGCTACTAAAGTTA
ATGTGTTTACTCTCTTTCTTCCACATTCTCAATTAAGGTGAGCTAAGCCTCCTCGGTG
TTTCTGATTAACAGTAAATCCTAAATCAAACCTGTTAAATGACATTTTTATTTTATGTCTC
TCCTTAACATAGAGACACATCTGTTTTACTGAATTTCTTTCAATATTCAGGTGATAGATT
TTTGTCTG

FIGURE 280

MYGKSSTRAVLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVT
WNFRPLDGGPEQFVFYYHIDPFQPMGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQ
VKNPDPDVGVIIEIRLSVVHTVRFSEIHFLALAIGSACALMIIIVVVVLFQHYRKKRWAER
AHKVVEIKSKEEERLNQEKKVSVYLETD

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FIGURE 281

GCATTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCATGAAGTTCTTAGCAGTCCTGGT
ACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCAGAATCCGACAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCTGATGCTGAAACCACTGCTGCT
GCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG
TAAAGACATTCCAGTTTACCCAAATGGGTGGGGATCTCCCGAATGGTAGAGTGTGTCCCT
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACATATTCATGCTTCTGTGATTTT
ATCCAACACTACTACCTTGCTTACGATATCCCTTTATCTCTAATCAGTTTATTTTCTTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

282/330

FIGURE 282

MKFLAVLVLLGVSI FLVSAQNPTTAAPADTYPATGPADDEAPDAETTAAATTATTAAPTAT
TAASTTARKDIPVLPKWVGDLPNGRVCP

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FIGURE 283

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGACCC
CTAGGGGTCTGGATTGTCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGAATGC
TACCTCCTGCCCTTCCACCTGCCCTGGTGTTCACGGTGGCCTGGTCCCTCCTTGCCGAGAGA
GTGTCTTGGGTCAGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTGTGTACCGAGAGGAC
ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG
GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGGCCAGTCCAGGGTGGGGGGCG
GCAAACCTCCATAAAGAACCAGAGGGTCTGGGCCCGGCCACAGAGTCATCTGCCAGCTCCT
CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAGTAAACACAGGCTGG
ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA
CCCCAAGAGCTTTCATTGTATCTATTGATTTTACCACATTAGCAATTAACCTGAGAAAT
GGGCCGGGCACGGTGGCTCAGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT
CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTACTAAAAA
TACAAAAAATTAGCCAGGCACAGTGGTGTGCACCTGGTAGTCCCAGTTACTCGGGAGGCTGAG
GCAGGAAAAATCGCTTGAACCCAGGAGGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT
TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

284/330

FIGURE 284

MLPPALPPALVFTVAWSLLAERVSWVRDAEDAHRLQPFVTERTLGKVQRWSGVHTQTGGRAG
GGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLCCWPGVGVARGGALCQ

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FIGURE 285

GTCATGCCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA
GCGGCCCCCATGGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCCCTGCTCTTCCATGG
GACCCCTGCAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGCTGACAA
AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTCAGC
CGGGGCCGGGATGCAGCCAGGAACCTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA
TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCAGGCACAGA
AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT
GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC
CCTCACAGGCCACGTGCAGCGGCAGAGGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC
AGATCCAGGAGAGACTCCACACAGCGGCGCTCCAGCCTGAATCTGCCTGGATGGAAGTGA
GACCAATCATGCTGCAAGGAACACTTCCACGCCCCGTGAGGCCCTGTGCAGGGAGGAGCTG
CCTGTTCACTGGGATCAGCCAGGGCGCCGGGCCCCACTTCTGAGCACAGAGCAGAGACAGAC
GCAGGCGGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAAGGACATGTA
CCCTTTTATGCTACACACCCCTCATTAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

286/330

FIGURE 286

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLLFHGTLLGQALNGVYRTTEGRLTK
ARNSLGLYGRRTIELLGQEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAAQQHRLRQ
IQERLHTAALPA

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FIGURE 287

GGCAACATGGCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAATGGACTTGTAATTTGCAT
 CCTGGTGATCACCTTACTCCTGGACCAGACCACCAGCCACACATCCAGATTAAAAGCCAGGA
 AGCACAGCAAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTTAAAAGCTC
 TGGACAGAAGTCAATGCCTTGAAGGAAATTCAGGCCCTGCAGACAGTCTGTCTCCGAGGCAC
 TAAAGTTCACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCCATGAGGCCAATG
 AAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCCAGGAACCTCCGACGAAATCAACGCC
 CTCCAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGA
 CATGGTCACGGAAGGCAAGTTTGTGACGTCAACGGAATCGCTATCTCCTTCTCAACTGGG
 ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAAACGTGTCTCTTCTCCCAATCAGCTCAG
 GGCAAGTGGAGTGATGAGGCCTGTCGCAGCAGCAAGAGATACATATGCGAGTTCACCATCCC
 TAAATAGAGTCTTTCTCCAATGTGTCTCCAAGCAAGATTATCATAACTTATAGGTTTCATGA
 TCTCTAAGATCAAGTAAAAATCATAATTTTACTTATTAATAAATTTGCAACACAAGATCAAT
 GTCCATAGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGCCCT
 TCCTGGGGTATAGGGGATCAGAAATATTTGATCCATGTGCACGCAGATAAAATGGCTTCTGTCT
 AAACAGACTAAAATCTTTCTCTAGTCTTTCTCACTTGTAACAACCCAGTTTGTGTTTCAA
 AATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT
 TTCCCTTGAAGTTTAGCGTATGTTTGACTAACAAAAATTCCTACATCAGAGACTCTAGGT
 GCTATATAATCCAAAAACTTTTCAGCCTGTGTCTCATTCTGTCCCATGCTGGCAATAATACC
 TTGTGAGCCCATACCCCTATTTTGAATTGCTCCATCTCCTGGTGGGACTTGTATCTTGTCT
 GCCATATCAGAACACAAACCCCTGAAGAGTTCTGATTGATTTTTTTTTTTTCTTCATGCC
 TACCCTTTTTTTGAAGTTTCCAGCCGCAATTTGAAATGAAATGACAAGGTGTATATTTGAT
 CAATTTTCATTCCCACCATTGCAATACAACCTCTAACTTAAATGGGTAAACCTAAGGCATAT
 CAAAGAAGCAGATTGCATGATAAACGGAATAGAAAAAAGAACCTACATTTATTTTGTCTT
 AGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCTTTTACATTT
 TCGTATATTTATTTTTTTTAGCCATCATTATATGTTTAAAGTCTATTATGGGCAACCAATCTT
 TGGAGCTGAAACGTAATTTAAAGAAATGCTATCTTGAAAATTGATACGTCTGTGCAATT
 TTTTATTCTGCCTAGTGTCTATTCTGCTTGTTTAACTAGATTGTACAAAATAACTTCATTGCT
 TAATATCAAATTACAAAGTTTAGACTTGAGGGGAAATGGGCTTTTGTAGAAGCAACAATTTT
 AAATATATTTTGTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTGTGAACAATAT
 CCCACTTGCAAACTTTAACTACACATGCTTGGAAATTAAGTTTGTAGCTGTTTTCATTGTCTCA
 ATAATAAGCCTGAATTCGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHSKRRVRDKDGDLLKTQIEKLWT
EVNALKEIQALQTVCLRGTKVHKCKYLASEGLKHFHEANEDCISKGILVIPRNSDEINALQ
DYGKRSPLGVNDFWLGINDMVTGKFDVNGIAISFLNWDRAQPNGGKRENCVLFSQSAQGK
WSDEACRSSKRYICEFTIPK

FIGURE 289

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGCGC
CCCGAGCCCCCGCGCCATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCTCTGCA
GCTCCGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCTGTCGCTGCGCTG
GAGTCGGCGGCGGAGGCCGGGGCCGGGACCTGGCCAACCCCTCGGCACCCCTCAACCCGCT
GAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGT
GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG
GCCCTGACAGTGTTTGGCTGAGCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC
CACCCGCGAGGGCTGAAAACCCCGCCGCGGGGAGGACCGTCCATCCCCTTCCCCGCGCCCT
CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
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MKLAALLGLCVALSCSSAAAFVGSAPVAPVAALESAAEAGAGTLANPLGTLNPLKLLLS
SLGIPVNHLEIGSQKCVaelGPQAVGAVKALKALLGALTVFG

FIGURE 291

TGAAGGACTTTTCCAGGACCCAAAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCACT
 CCTTGGCTCCGCAGCCGATCACA**ATGA**AGGTGGTGCCAAGTCTCCTGCTCTCCGTCTCCTCTG
 GCACAGGTGTGGCTGGTACCCGGCTTGGCCCCAGTCTCAGTCGCCAGAGACCCAGCCCC
 TCAGAACCCAGACCAGCAGGGTAGTGACGGCTCCCAGGGAGGAAGGAAGATGAGCAGGAGG
 CCAGCGAGGAGAAGGCCGTGAGGAAGAGAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTT
 GCCAAGGAGACTTCAAACCTTCGGATTGAGCCTGCTGCGAAAGATCTCCATGAGGCACGATGG
 CAACATGGTCTTCTCTCCATTTGGCATGTCTTTGGCCATGACAGGCTTGATGCTGGGGGCCA
 CAGGGCCGACTGAAACCCAGATCAAGAGAGGGCTCCACTTGAGGCGCTGAAGCCCAACAAG
 CCCGGCTCCTGCCTTCCCTCTTAAAGGGACTCAGAGAGACCCTCTCCCGCAACCTTGAACCT
 GGGCCTCTCACAGGGGAGTTTTCCTTTCATCCACAAGGATTTTGATGTCAAAGAGACTTTCT
 TCAATTTATCCAAGAGGTATTTTGATACAGAGTGCGTGCTATGAATTTTCGCAATGCCTCA
 CAGGCCAAAAGGCTCATGAATCATTACATTAACAAAGAGACTCGGGGGAAAATTTCCCAAACCT
 GTTTGATGAGATTAATCCTGAAACCAAATTAATTTCTTGTGGATTACATCTTGTTCAAAGGGA
 AATGGTTGACCCCATTTGACCTGTCTTACCAGAGTCGACACTTTCCACCTGGACAAGTAC
 AAGACCATTAAAGTGCCCATGATGTACGGTGACGGCAAGTTTGCCCTCCACCTTTGACAAGAA
 TTTTCTGTTGTATGTCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCA
 TGGAGAAAATGGGTGACCACCTCGCCCTTGAAGACTACCTGACCACAGACTTGGTGAGACA
 TGGCTCAGAAACATGAAAACCAGAAACATGGAAGTTTCTTCCGAAGTTCAAGCTAGATCA
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAAATCTTCTACCCCTTTG
 CTGACCTTAGTGAACTCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTACGAAGA
 ACAGTGATTTGAAGTTGATGAAAGGGGCACTGAGGCAGTGCCAGGAATCTTGTGAGAATTAC
 TGCTTATTTCCATGCCTCTGTCTCAAGTGGAACCGGCCATTTTCATTTATGATCTATGAAG
 AAACCTCTGGAAAGCTTCTGTTTCTGGGCAGGGTGGTGAATCCGACTCTCCTAT**TAA**ATTCAAG
 ACATGCATAAGCACTTCTGTCTGTAGTAGATGCTGAATCTGAGGTATCAACACACACAGGA
 TACCAGCAATGGATGGCAGGGGAGAGTGTTCCCTTTTGTCTTAACTAGTTTAGGCTGTTCTC
 AAATAAATACAGTAGTCCCCACTTATCTGAGGGGGATACATTCAAAGACCCCCAGCAGATGC
 CTGAAACGGTGAGCAGTGCTGAACCTTATATATATTTTTTCTTACATACATACCTATGAT
 AAAGTTTAATTTATAAAATTAGGCACAGTAAGAGATTAACAATAATAACAACATTAAAGTAAAA
 TGAGTTACTTTGAACGCAAGCAGTGCATATACCATAACAGTCAAACCTGATTATAGAGAAGGCTA
 CTAAGTGACTCATGGCGAGGAGCATAGACAGTGTGGAGACATTTGGCAAGGGGAGCAATTCA
 CATCCTGGGTGGGACAGAGCAGGACGATGCAAGATTCCATCCCACTACTCAGAAATGGCATGC
 TGCTTTAAGACTTTTAGATTGTTTATTTCTGGAATTTTTCATTTAATGTTTTTGGACCATGGT
 TGACCATGGTTAACTGAGACTGCAGAAAGCAAACCATGGATGAAGGAGGACTACTACAAAA
 GCATTAAATTGATACATATTTTTTAAAAAAAAAAAAAAAAAAAA

FIGURE 292

MKVVP S L L L S V L L A Q V W L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E E K A G E
E E K A W L M A S R Q Q L A K E T S N F G F S L L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I
K R G L H L Q A L K P T K P G L L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F
D T E C V P M N F R N A S Q A K R L M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P
V F T E V D T F H L D K Y K T I K V P M M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V V L M E K M G D H L
A L E D Y L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A
T G R N L Q V S R V L R R T V I E V D E R G T E A V A G I L S E I T A Y S M P P V I K V D R P F H F M I Y E E T S G M L L F
L G R V V N P T L L

FIGURE 293

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCCAGACATGAG
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGTGTGGGAGGCAGGTGCAGTCCCAG
CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGCTGTTCCC
TGTCAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTCAGGGCAGGGGCCCA
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCCTGGGCCGTGTCTGAGTCCC
GAGCCCACCATGACAGCCTGTACCACCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCC
CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACA
TCTACCACCCCAGTAGGGCTCCAGGGGCCATCACTGCCCCGCCCTGTCCCAAGGCCAGG
CTGTTGGGACTGGGACCCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCAGCAGGCAAA
AAAAAAAAAAAAAAAA

FIGURE 294

MRRLLVTSLVVVLLWEAGAVPAPKVPIKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVL
FPVQPKKLLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPFEEDQGEE
RPRLWVMPNHQVLLGPEEDQDHIYHPQ

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FIGURE 295

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGAGGGAGGGAGTGGAAGGAGCTCTCTG
TACCAAGGAAAGTGCAGTGCAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCTCTGC
TGTTTCTCATAGCGACCACAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
TGGACCTGTTCTTCGTCTCCATCTCTGCCAGAAAGCTGCAAGGAAATCAAAGACGAATGTCC
TAGTGCAATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCT
GTGACATGACCTCTGGGGGTGGCGGCTGGACCTGGTGGCCAGCGTGCATGAGAATGACATG
CGTGGGAAGTGCACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC
AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCG
ATGACTACAAGAACCCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG
CCCAATAAGTCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC
TGGCTTCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAAT
ATGGAGAAGGAAAGTGTGGACTGACAACGCCCCGGTGATCCCTGTGGTCTATGATTTTGGC
GACGCCAGAAACAGCATCTTATTACTCACCCATATGGCCAGCGGGAAATCACTGCGGGATT
TGTTCAGTTTCAGGGTATTTAATAACGAGAGAGCAGCCAACGCCCTTGTGTCTGGAATGAGGG
TCACCGGATGTAACACTGAGCATCACTGCATTTGGTGGAGGAGGATACTTTCCAGAGGCCAGT
CCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATATGGAACCATGTTGGTTA
CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTGAGAGTTTTGTG
GGAGGGAACCCAGACCTCTCTCCCAACCATGAGATCCCAAGGATGGAGAACAACCTTACCCA
GTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGAAAAAAA

FIGURE 296

MNQLSFLFLFIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN
GVYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFG
SAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGI
YQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYYSYPYGQREFTAGFVQFRVFNNERAAN
ALCAGMRVTGCNTEHHCIGGGGYFPEASPQCGDFSGFDWSGYGTHVGYSSSREITEAAVLL
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FIGURE 297

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCACCTCGGCTGGGAGCC
 CACGAGGCTGCCGCATCCTGCCCTCGGAACAATGGGACTCGGCGCGCGAGGTGCTTGGGCCG
 CGTGCTCCTGGGAGCGCTGCAGGTGCTAGCGCTGCTGGGGCCGCCCATGAAAGCGCAGCC
 ATGGCGGCATCTGCAAAACATAGAGAATTCTGGGCTTCACACAACCTCCAGTGCTAACTCAAC
 AGAGACTCTCCAACATGTGCCCTTCTGACCATACAAATGAAACTTCCAACAGTACTGTGAAAC
 CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG
 GCATCTAATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC
 TACACCCAAAACAACAAGTGTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG
 TAACCCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAACATATGCAT
 TCTGAAGCAAAGAAAGGATCAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAAC
 GCTGGGAGTTTTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATT
 GGTATCGAACCATAGATGAACATGATGCCATCATTTAAGGAATCCATGGACCAAGGATGGA
 ATACAGATTGATGCTGCCCTATCAATTAATTTTGGTTTATTAATAGTTTAAACAATATTCT
 CTTTTTGAAAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAATATGTA
 AAGATTCTCAAGGTAACAAGGGTTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGT
 TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAAACAAGTCCTATCTTTTTTTTTGGCT
 GGGGTGGGGCATTGGTCACATATGACCAAGTAATTGAAAGACGTCATCACTGAAAGACAGAA
 TGCCATCTGGGCATACAAATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTTGT
 AGCTCACATAAAGAACTTCAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA
 CAGAAATTATACAATCAAACTAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTG
 TGCTTTAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

CACGCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCGAGCCGGAGCGCCG
TCGCGGGGGCTCCGGGCTGTGGGACCCTGGGCCCCAGCGCATGGCGACCCCTGTGGGAGGC
CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTCCGTGCTGCTGCTGGC
GCAGCTGTCAGACGCCGCCAAGAATTTGAGGATGTCAGATGTAATGTATCTGCCCTCCCT
ATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTT
CATGTTGTGGAGCCCATGCCCTGTGCGGGGGCCTGATGTAAGAAGCATACTGTCACGCTGTGA
ATGCAAAATATGAAGAAAGAAGCTCTGTCACAATCAAGTTACCATTTATAATTTATCTCTCCA
TTTTGGGCCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG
CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT
TGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTAG
AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGG
CATGTTGTCTCAGCTTAATTTGGGAATGTAATTCAGGTGACTAGAAGAAACAGGCAGACAA
CTGGGAAGAAGTACTGGGTTTGTGCTGGGTTTCATTTTAATACCTTGTTGATTTACCAACT
TGTGCTGGAAGATTCAAAGCTGGAAGCAAAACCTGCTTGATTTTTTTTCTTGTTAAAGTA
ATAATAGAGACATTTTTTAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCTATTTG
TGACTTTTACTAATAAAAAATAAATCTGCCTGTAAATTATCTTGAAAGTCCTTTACCTGGAACA
AGCACTCTCTTTTTTACCACATAGTTTTAACTTGACTTTCAAGATAAATTTTCAGGGTTTTTG
TTGTTGTTGTTTTTTGTTGTTGTTGTTGTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGTT
AACAACCTTTTTTCAAGTCACTTTACTAAACAACTTTTGTAATAGACCTTACCTTCTATTG
TCGAGTTTCATTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTG
ACTTTTGCAGTGACTGTATTATCTGGGTATCTGCTGTGTCGACTTCATGGTAAACGGGAT
CTAAATAGCTGGTGGCTTTTACAAAAAGCAGATTTTTCTTCATGTACTGTGATGCTGTATG
CAATGCATCCTAGAACAAACTGGCCATTGCTAGTTTACTCTAAAGACTAAACATAGTCTTG
GTGTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACT
TGCAATAAAGAAATTTTATTTTAAAGCCCAAGCTCCCTGGATTGATAATATATACACATTG
TCAGCATTTCCGGTGTGGTGGAGCGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACT
AGGGCTGGGCTGTGGTGGCTCTTCTGAAAGGCTCAACCATTTATGGTAAGTCTGGCTTTT
TCTTCTCATGTCTCTCTTTGGAATGTAAACAATAAAAAATAATTTTGAACATCAA

MATLWGGLRLRGLSLSLSCALSVLLLAQLSDAAKNFEDVRCKICPPYKENGHIYKNKIS
 QKDCCLHVVEPMPVRGPDVEAYCLRCECKYEERSSVTIKVTIIYLSILGLLLLYMYVLT
 VEPILKRRLFGHAQLIQSDDDIGDHQPFAHAHDVLARSRSRANVLNKVEYAQQRWKLQVQEQ
 RKSVDHRHVLS

FIGURE 301

GCACCTGCGACCACCGTGAGCAGTCATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT
CTGGGCTTGTCTGGCTCTGTGCTGCTGCCAAGGCCTTCTGTCCCGCGGAAGCGG
CAGGAGCCGCCGCCGACACCTGAAGGAAAAATTGGGCCGATTTCACCTATGATGCATCATCA
CCAGGCACCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGG
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGAGAGAGGTCTG
ATGGGGCAGATTATTCCAATCTACGGTTTTTGGGATTTTTTTATATATACTGTACATTCTATT
TAAGGTAAGTAGAATCATCCTAATCATATTACATCAATTGAAAATCTAATATGGCGATAAAAA
TCATTGTCTACATTAAACTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTA
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTTCAGTTTCACATAAGAATG
TTTACTCAATGTTTTAAGTGTTTTGCCCCAAAATTCACAACCTACAAGGCAGAACTAGGACTT
GAACATGGATCTTTTGGTTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

[illegible]

Mathematical Induction

FIGURE 303

CGGCTCGAGTGCAGCTGTGGGGAGATTTCAGTGCATTGCCTCCCCGGGTGCTCTTCATCTT
 GGATTTGAAAGTTGAGAGCAGCATGTTTTGCCCCACTGAAACTCATCTGCTGCCAGTGTTAC
 TGGATTATTCCTTGGGCTGAATGACITGAATGTTTCCCCGCCTGAGCTAACAGTCCATGTG
 GGTGATTCAGCTCTGATGGGATGTGTTTCCAGAGCACAGAAGACAAATGTATATTTCAAGAT
 AGACTGGACTCTGTACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCA
 ATCTCAGTGTGCCTATTGGGCGCTCCAGAACCGGTACACTTGATGGGGACATCTTATGC
 AATGATGGCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA
 AATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAG
 AGGAGCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTAGATGGGATGTGTTTCCAG
 AGCACAGAAGTGAAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGA
 GGAGATTGTATTTCTGTACTACCACAACTCAGGATGTCTGTGGAGTACTCCCAGAGCTGGG
 GCCACTTCCAGAATCGTGTGAACCTGGTGGGGACATTTTCCGCAATGACGGTTCCATCATG
 CTTCAGGAGTGAGGGAGTCAGATGGAGGAAACTACACTGCAGTATCCACCTAGGGAACCT
 GGTGTTCAAGAAAACATTGTGCTGCATGTGAGCCCGAAGAGCCTCGAACACTGGTGACCC
 CGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTTGTGGGAATTGTCT
 TGTGCCACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAATAA
 GAGTTTCAGTGAATTCTACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAG
 AAAAACCTTGCATTTTGAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTA
 CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAGGACACATTTACTCCCCAATAATTGTA
 CCCAGTTTGGCCTTCTCTGAGGTCAGATCGGAACAACCTCACTTGAAGAAAAGTCAGGTGGGG
 GAATGCCAAAAACACAGCAAGCCTTTTGAAGAAGATGGAGAGTCCCTTCATCTCAGCAGCGG
 TGGAGACTCTCTCTGTGTGTGCTCGGGCCACTCTACCAGTGATTTTCCAGACTCCCGCTCTC
 CCAGCTGTCTCTGTCTCATTGTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGG
 CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGC
 CTCTGGAGTGGGACACTGGCCCTGGGAACAGGCTGAGCTGAGTGGCCTCAAACCCCCGTT
 GGATCAGACCTTCTGTGGGCAGGGTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATA
 AAAACCAACCCAAATCAA

FIGURE 304

MFCPLKLILLPVLLDYSGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSPG
EHAKDEYVLYYNSLVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYYICEIRLKGES
QVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYY
HKL RMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRES DGGNYTCSIHLGNLVFKKTIV
LHVSPEEPRTLVT PAALRPLVLGGNQLVIIVGIVCATILLPVLILIVKKT CGNKSSVNSTV
LVKNTKKTNP EIKEK PCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPVWPSLR
SDRNN SLEKKSGGMPKTQQAF

FIGURE 305

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATG
GTTCTACCCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG
AAACTACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCC**ATG**CA
GGATGAAGATGGATACATCACCTTAAATATTAAAACTCGGAAACCAGCTCTCGTCTCCGTTG
GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG
ATGGTTGTGCGGGCTGGTGGCTCTGGGGATTTGGTCTGTGCATGCAGCGCAATTACCTACAAGA
TGAGAATGAAAATCGCACAGGAACTCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG
TAAAACAATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCTGTGACACAAAC
TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACTTAACATGGGAAGAGAG
TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG
AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAAT
GAGGTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAAATATGTTTGAGTTTTTGGAAGA
TGGAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCTACCTTCTGTG
AGAACAAACATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT
TAATGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAGATATGT
ATGAATGCATCAGTAGCTGAAAAAAAAAAAAAA

306/330

FIGURE 306

MQDEDGYITLNIKTRKPALVSVGPASSSWWRVMA LILLILCVGMVVGLVALGIWSVMQRNYL
QDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDS CYGFFRHNLWE
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMF EFL
EDGKGNMNCAYFHNGKMHPTFCENKHLYLMCERKAGMTKVDQLP

090906Z JAN 61
FM 44TH AFHQ
TO 44TH AFHQ

FIGURE 307

CCCACGCGTCCGCGCAGTTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCGCATCCCGG
CCCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCCGACCGC
CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTGC GGAGAA
GCCCCGGCAAACGCAGGCTAAGGAGACCAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAG
CGGAGGAGAAGGAGGAGGAGGCGAACCAGAGAGGGGCAGCAAAAGAAGCGGTGGTGGTGGG
CGTCGTGGCC**ATG**GCGGCGGTATCGCCAGCTCGCTCATCCGTGAGAAGAGGCAAGCCCGCG
AGCGCGAGAAATCCAACGCCTGCAAGTGTGTGAGCAGCCCCAGCAAAGGCAAGACCAGCTGC
GACAAAAACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG
AAGAAGACCAGAGCCTCAGCTTAAGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC
ACTTGCAGCTGCAGGCGGATGGAACCATTTGATGGCACCAAGATGAGGACAGCACTTACACT
CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACCTTTTACACCTGAGTGCA
AATTCAAAGAATCAGTGTTTGAAAATTATTATGTGACATATTATCATCAATGATATACCGTCAG
CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGT
ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGACCCCAACC
AAGAGCAGAAGTGTCTCTGGCGTGCTGAACGGAGGCAAATCCATGAGCCACAATGAATCAAC
G**TAG**CCAGTGAGGGCAAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT
TCTTCTAGCAGTCCTTACCCAAAAGTTCAAATTTGTGAGTGACATTTACCAAAACAAACAGG
CAGAGTTCACTATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

FIGURE 308

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498

><subunit 1 of 1, 245 aa, 1 stop

><MW: 27564, pI: 10.18, NX(S/T): 1

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGTSCDNKLNVFSRVKLFSGSKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA
MNSEGILYTSSELTPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLENKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGG
ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG
CAACCTGGATATTCTGAGACATATTTTGGGGGATTTTCAGTGAAAAAGTGGGGGATCCCT
CCATTAGAGTGTAGCAAAGGAAAAACACCAAGGTTGGGTTCCCTTCTGACATTGGCAGTG
CCCCAGTAGGGGTGGGATGAGCGAATATTCCCAAAGCTAAAGTCCCACACCTGTAGATTAC
AAGAGTGGATTTGTCAGGAGTGTGCCCCAAAATACAGTGGAAAGGTGCCTGAAGATATTTAA
ACCACGCTCTTGGAATTTAGTGGGCTTTGGCTTTGGGATAGGTGAAGTGAGGACAGACACTG
GAGAGGAGGGAAGGGGGACGTTTTCAATAGGAGGCAAACTCGAGGTTGGGATCCACTGAGG
AGTACATAGGCTGCTGGATTCTGGTGGAGCCAGCACTGGGCCACGGGTGTTAACTGGCTGCT
GTGGAGGGGGGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCCTGTGGGTGGGGCAG
CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCAG
CGCGCTCCGGGCCTGCCGTTTGGGGGTGTCTCCTCCCGGGCGCTATGCGCGCGCTGGC
CAGTAGCCTGATCCGGCAGAAGCGGGAGGTCCGCGAGCCCGGGGGCAGCCGCGCCGTTGTCGG
CGCAGCGCGCGTGTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCTCG
CTGTCCAAGGTGCGAGTGTGCGGGGGGGCGGCCCGCGCGGCCGGACCGCGGCCCGGAGCCTCA
GCTCAAAGGCATCGTCACCAAAGTGTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCG
ACGGAAGCATCCAGGGCACCCAGAGGATACAGCTCCTTCAACCACTTCAACCTGATCCCT
GTGGGCCTCCGTGTGGTCAACATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC
TGAGGGACTGCTACAGTTCGCCGCAATTTACAGCTGAGTGTGCTTTAAGGAGTGTGTCT
TTGAGAATTACTACGCTCTGACGCTCTAGCTCTCTACCGCCAGCTGCTTCTTGCCCGGGC
TGGTACCTCGGCCTGGACAAGGAGGCCAGTCAATGAAGGAAACCGAGTTAAGAAAGACCAA
GGCAGCTGCCACTTTCTGCCCAGGCTCTCGGAGGTGGCGGATACAGGAGGATCTTCTTC
ACAGTGTCCCCGAGGCCTCCCCTTCCAGTCCCCCTGCCCCCTGAAGTGTAGTCCCTGGACTG
GAGGTTCCCTGCACTCCAGTGAGCCAGCCACCACCACAACCTGT

MAALASSLIQKREVRPEGSGRPVSAQRRVCPRGTKSLCQKQLILLISKVRLCGGRPARPDR
GPEPQLKGIIVTKLFCRQGFYQLQANPDGSIQGTPEDTSSFTFNLIPIVGLRVVTIQSAKLGHY
MAMNAEGLLYSSPHFTAECRFKECVFENYVYLYASALYRQRSSGRAWYLGLDKEGQVMKGNR
VKKTKAAAHFLPKLLEVAMYOEPSLSVPEASPSPPAP

amino acids 199-207

amino acids 54-60, 89-95, 131-137

amino acids 131-155

ATGCGCCGCGGCATCGTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGGGAGCAGCACTG
GGACCGCCGCTGTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACC GGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGATATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAAATGCACCCGATGGAGTCTCGATGGAACCAAGGATGACAGCCTAATTCTACACTCT
TCAACCTCATACCAAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTGGGATTAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA
GTAAAGAAAACCAACAGCAGCTATTTCCTACCCAGCCATTGGAAGTTGCCATGTACCG
AGAACCATTCTTGACATGATGTTGGGGAACGGTCCCGAAGCCTGGGTTGACGCCAAGTAAAA
GCACAAGTGCCTCTGCAATAATGAATGGAGGCAACCGATCAACAAGAGTAAGACAACATAG

FIGURE 312

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWDRPSASRRRSSPSKNRGLCNGNLVDIFSKVRIFGLKKRRLR
RQDPQLKGIVTRLYCRQGYYLQMHDPGALDGTKDDSTNSTLFLNLPVGLRVVAIQGVKTGLY
IAMNGEGYLYPSELFTECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKSSTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

FIGURE 313

GGGGAGAGGAATTGACCATGTAAAGGAGACTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAAAT
 GAAGGATGACGAGACGAGCTTTCTCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGA
 ACGAAGCTTTTTCTTGTGAGCCCTGGATCTTAACACAAATGFGTATATGTGCACACAGGGAGCATTCAAGAAATG
 AAATAAACCCAGAGTTAGACCCGCGGGGGTGGTGTGTTCTGACATAAATAAATAATCTTAAGCAGCTGTTCCCT
 CTCCCCACCCCCAAAAAAGGATGATTGGAATGAAGAACCGAGGATTCAACAAAGAAAAAGTATGTTCAATT
 TTCTCTATAAAGGCAAAAGTGAGCCAGGAGATATTTTGGAAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAA
 AGAACTGGTGGTGGTGGTGGTCTTTCTTTCTTTGAATTTCCCAACAGAGGAGAGGAAATTAATAATACATCTGC
 AAAGAAATTTAGAGAAAGAAAGTTGACCGCGGAGATTGAGGCATTGATTGGGGGAGAGAAACCGAGAGCA
 CAGTTGGATTGTCCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTTCTTCATCAACCTCCTTT
 TTTTAAATTTTTATCTCTTTGGTATCAAGATCATGCGTTTTCTCTGTTCTTAACCACTGGATTCCATCT
 GGATGTTGCTGTGATCAGTCTGAATACAACCTGTTGAATCCAGAAGGACCAACACAGATAAATTAATGAATG
 TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGTCTAGGTTTAAACAGGGCCCTATTTGACCCCT
 GCTTGTGGTGTGCTGGCTCTTCACTCTCTTGTGGTGGTGGTCTGGTGGGGCTCAGACCTGCCCTCTGTGT
 GCTCCTGCAGCAACAGGTTGAGCAAGGTGATTGTGTTGGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCC
 ACCAACACACGGCTGCTGAACCTCCATGAGAACCAATCCAGATCATCAAGTGAACAGCTTCAAGCACTTGAG
 GCACTTGAAGTCTCAGCTTGGTAGTAGGAACCATATCAGAACCAATTGAATTTGGGGCTTTCAATGGCTTGGCGA
 ACCTCAACACTCTGGAACCTTTGACAATCGTCTTACTACCATCCGGAATGGAGCTTTGTATACTTGTCTAAA
 CTGAAGGAGCTCTGGTTCGGAACAACCCCAATTGAAAGCATCCCTCTTATGCTTTTAAACAGAATTCCTTCTTT
 GCGCCGCTAGACTTAGGGGAATGAAAAGACTTTCATACACTCAGAAGGTGCGTTTGAAGGTCTGTCCAAT
 TGAGGTATTTGAACCTTGCCATGTGAACCTTCGGGAATCCCTAACCTCACACCGCTCATAAACTAGATGAG
 CTGGATCTTTCTGGGAATCATTATCTGCCATCAGGCCTGGCTCTTCCAGGGTTTGTATGCACCTTCAAAACT
 GTGGATGATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCCTTGACAACCTTCAGTCACTAGTGGAGATCA
 ACCTGGCACAAATACTAATCTTACTGCTCATGACCTCTTCACTCCCTTGACATCATAGAGCGGATACAT
 TTACATCAACCCCTTGGAACTGTAACTGTGACATACTGTGGCTCAGCTGGTGGATAAAGACATGGCCCCCTC
 GAACACAGCTTGTGTGCCCCGTGTAACTCTCTCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGA
 ATTACTTCAATGCTATGCTCCGGTATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCT
 GAGCTGAATGTGCGGCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCATGACACA
 TGGGGCTACAAGTGGGATAGCTGTGCTCAGTGATGGTAAATTTACAAATGTAAGTCACTGGCTGTGCAAGATA
 CAGGCATGTACACATGTATGGTGGTAAATTCGGTGGGAATACTACTGCTTCAAGCCCTGAAATGTTACTGCA
 GCAACCACTACTCCTTTCTTACTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCAGG
 GACCACAGATAAACAATGTGGTCCCATTCCAGTGGTGCAGTGGGAGACCACCAATGTGACCACCTCTCTCACAC
 CACAGAGCACAGGTCGACAGAGAAAACCTTCAACATCCCAGTACTGATATAAACAGTGGGATCCCGGAAT
 GATGAGTCAATGAAGCTACCAAAATCATCATTGGGTGTTTGTGGCCATCACATCTAGGCTGCAGTGATGCT
 GGTCAATTTCTACAAGATGAGGAAGCAGCACCATCGGCAAAACCATCACGCCCAACAGGACTGTTGAAATTA
 TTAATGTGGATGATGAGATTACGGGAGACACACCATGGAAGGCCACTGCCATGCTGCTATCGAGCATGAG
 CACCTAAATCACTATAACTCATACAATCTCCCTCAACCACACAACAACAGTTAACACAATAAATTCATATCA
 CAGTTGAGTCATGAACCGTTATTGATCCGAATGAACCTTAAGACAATGTACAAGAGACTCAAACTTAAACAA
 TTTACAGAGTTACAAAAACAAACAATCAAAAAAAGACAGTTTATTAAAAATGACACAATGACTGGGCTAA
 ATCTACTGTTCAAAAAGTGCTTTACAAAAAACAAAAAGAAAGAAATTTATTATTAAAAATCTATTG
 TGATCTAAGCAGACAAAAA

FIGURE 314

MLNKMTLHPQQIMIGPRFNALFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVDPDGISTNTRLNLHENQIQIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLMTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLYLNAMCNLREIPNLTPLIKLDELDSLGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHHLHNPWNCNDIL
WLSWWIKDMAPSNTACCARCNTPPNLIKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVDQTMGYTCMVNSVGN
TTASATLNVTAATTTFFSYFSTVTVTETMEPSQDEARTTDNNVGPTPVVDWETTNTVTSITPQ
STRSTKFTFTIPVTDINSIGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDDEITGDTPMESHLMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 315

GCGCCGGGAGCCCATCTGCCCCAGGGGACGCGGGCGCGGGGCCGGCTCCCGCCCGGCACAT
 GGCTGCAGCCACCTCGCGCGCACCCCGAGGCGCGCGCCAGCTCGCCCGAGGTCGGTCCGA
 GCGCCCGCGCGCGCCCGGAGCCAAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATC
 GGG**ATG**TCCCTCCTCTCTCTCTCTTGTCTAGT**TT**CCTACTATGTTGGAACTTGGGGACTCA
 CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTGCCTGCCACCATCAACTGGGGC
 TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCAGTAATGAAGGGAAACAAAAA
 GTGGTGATCACTTACTCCAGTCGTCATGTCTACAATAACTTGACTGAGGAACAGAAAGGCCG
 AGTGGCCCTTTGCTTCCAATTTCTGGCAGGAGATGCCTCCTTGCAGATTGAACCTCTGAAGC
 CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTGAGGGCCCTACGTGTGGAGCCAT
 GTCATCTTAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTGTGAAGGAGAGCTGAC
 AGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTTGTGATTT
 ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCTCCCAATCTAGGATT
 GACTACAACCCACCTGGACGAGTTCTGCTGCAGAAATCTTACCATGTCTACTCTGGACTGTA
 CCAGTGACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCAGTAAGTGTACAGT
 ATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG
 ATTTTCTCTTTGGTGTGGCTGCTAATCCGAAGGAAAGCAAAAGAAAGATATGAGGAAGAAAGA
 GAGACCTAATGAAATTGAGAAAGATGCTGAAGCTCCAAAAGCCCTCTTGTGAAAACCCAGCT
 CCTCTTCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCTCCACTCGCTCCACAGCAAT
 AGTGCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCCGAGCCAGGGCTGGCCAC
 CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACCATG
 CTAATCTGACCAAGCAGAAACACACCCAGCATGATCCCGAGCCAGAGCAGAGCCTTCCAA
 ACGGTC**TGA**ATTACAATGGACTTGACTCCCACGCTTTCTTAGGAGTCAGGGTCTTTGGACTC
 TTCTCGTCATTGGAGCTCAAGTCACAGCCACACAACAGATGAGAGGTCATCTAAGTAGCA
 GTGAGCATTTGCAGGAACAGATTGAGATGAGCATTCTTCTTATACAATACCAACAAAGCAAA
 AGGATGTAAGCTGATTCATCTGTAAAAGGCATCTTATTGTGCCTTAGACAGAGTAAGGG
 AAAGCAGGAGTCCAAATCTATTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG
 AGGTGAATATACCTAAAACCTTTAATGTGGGATATTTTGTATCAGTGCTTTGATTACAAAT
 TTCAAGAGGAAATGGGATGCTGTTTGTAAATTTCTATGCATTTCTGCAAACCTATTGGATT
 ATTAGTTATTGACAGAGTCAAGCAGAACCCACAGCCCTATTACACCTGTCTACACCATGTAC
 TGAGCTAACCCTTCTAAGAACTCCAAAAAGGAAACATGTGCTTCTATTCTGACTTAAC
 TTCATTTGCTATAAGGTTTGGATATTAAATTTCAAGGGGAGTTGAAATAGTTGGGAGTAGGAGA
 AGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTGTATGTAGGCCCAAAATGAC
 TATGAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTCCACTCTTCTATGATGTT
 ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCTTCAAT
 CAGATGCCCTTAAGGACTTCTGCTAGATATTCTTGAAGGAGAAAAATACAACATGTCAAT
 TATCAAGCTCTTAGAAAGAATTCTTCTAGAGAAAAAGGGATCTAGGAATGCTGAAAGATTA
 CCCACATACCATTTAGTCTCTTCTTCTGAGAAAAATGTGAACAGAAATGCAAGACTGG
 GTGGACTAGAAAGGGAGATTAGATCAGTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA
 TGGTGCCAGGCTGTAGGAAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC
 ATTGCATCCAGCCTGGGTGACAGACGGGACTCCGTCTC

316/330

FIGURE 316

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLVSYYVGTGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELTEGSDLTLCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANS
ASRSQRTLSTDAAPQPLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPQSRAFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

[illegible]

318/330

FIGURE 318

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361

><subunit 1 of 1, 352 aa, 1 stop

><MW: 38938, pI: 7.86, NX(S/T): 3

MALLLLCFVLLCGVVDFAFARSLSIITPEEMIEKAKGETAYLPCKFTLSPEDQGGLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKK
APGVANKKIHLVVLVKPSGARCYPVDGSEEIGSDFKIKCEPKESLPLQYEWQKLSDSQKMPT
SWLAEMTSSVISVKNASSEYSCTYVNRVVGSDQCLRLNVVPPSNKAGLIAGAIIGTLL
ALALIGLIIFCCRKKRREEKYEKEVHHDIREDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM
EGYSKTQYNQVPSEDFERTPQSFPLPPAKFKYPYKTDGITVV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

FIGURE 319

TGAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGA
 ATGGTGAAGGTGCCTGTCTAATTTTTCTGTAAAAAGAACAGCTGCCTCCAGGCAGCCAGCC
 CTC AAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTCGC
 CAATTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG
 AGAGATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTTAGCCAGACCCCTTCTGCCCTC
 CTTTGCTGGCGACAGCCTCTCAAATGCAGATGGTGTGCTCCCTTGCTGGGTTTTACCCCTG
 CTTCTCTGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCACCTTTGGGCCCTGCCAAGT
 GAAGGGGGTGTGTCCCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG
 CTCAGGATAACATCACGAGTCCCCGGCTGCTGCAGCAGGAGGTCTGCAGAACGTCTCGGAT
 GCTGAGAGCTGTTACCTTGTCCACACCTGCTGGAGTTCTACTTGAAAAGTGTTTTCAAAAA
 CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACAAC
 TTGTTCTCATCGTGTCAACCTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGAC
 AGTGCACACAGGCGGTTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGC
 TCTGACCAAAAGCCCTTGGGGAAGTGGACATTCTTCTGACCTGGATGCAGAAATCTACAAGC
 TCTGAATGTCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTTGTTCCTGTGTCAATTTCA
 AACAGTCTCCCTTCTATGCTGTTCACTGGACCTTCACGCCCTTGGCCATGGGTCCCATTC
 TTGGCCCAGGATTATTGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG
 GTGCCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTTGATTTATTACAACCTATTTT
 AATTAAATGTCAGTATTTCAACTGAAGTTCTATTTATTTGTGAGACTGTAAGTTACATGAAG
 CAGCAGAATATTGTCCCCATGCTTCTTTACCCCTCACAATCCTTGCCACAGTGTGGGCGAG
 TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGTCTTTTTTTGGCCTGTCTTTGGATT
 GTTAAAAAACAGAGAGGGATGCTTGGATGTAAAAGTGAAGTTCAGAGCATGAAAATCACACT
 GTCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGGTAAAGTGCATCTGTTTGAAAAG
 TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCCTCAATAAACATTTTCATT
 TCCCACCCACACTGCAGCTCACCCATCATCCCTTTCCCTGGTGCCCTCCTTTTTTTTTT
 TATCCTAGTCATTCTCCCTAATCTTCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGAC
 ATTGACCTGGATGTACTATCCAATCTGTGATGACATCCCTGTCTAATAAAAGACAACATAA
 CTC CAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 320

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRLLQSLWTLARPFPCPELLATASQMOMVVLPCLGFTLLLSQVSGAQQQEFHFGPCQVK
GVVPQKLWEAFWAVKDTMQAQNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLKTVFKNH
HNRTVEVRTLKSFSTLANNFVLIVSQIQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAAL
TKALGEVDILLTWMQKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

FIGURE 321

AAGGAGCAGCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTT
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCACTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAAGGATCA
TCAGGAGCCAAACCCCAAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCCTCTACA
TGCAGAAAACCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGTCTTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT
GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGAAGGCCCTTGACAGCTGAAAGTCC
CACTGGCTGGCCTCAGGCTGTCTTATTCGCTTGAAAATAGGCAAAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATCCATATTTTACCTATGA

FIGURE 322

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282
><subunit 1 of 1, 177 aa, 1 stop
><MW: 20452, pI: 8.00, NX(S/T): 2
MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEI KRAIQAKDTFPNV TILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHNDYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

FIGURE 323

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG
AACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTAT
AGAATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAACCTGCACCTC
GGTTCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCACCGATGTTGGGGGCCCGCCT
CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCTCAGAGCCTATCCCA
ATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCC
AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC
CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA
TGAGCAGAAGATACCTCTGCATGGATTTAGAGGCAACATTTTGGATCACACTATTTGAC
CCGGAGAAGTGCAGGTTCCAAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACCTCTCC
TCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACC
CACCCCGTACTCCAGTTCTCTGTCCTCCGAGGAACGAGATCCCCCTAATTCACTTCAACACC
CCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCTGAACGT
GCTGAAGCCCCGGGCCCGGATGACCCCGGCCCGGCCCTCCTGTTTACAGAGAGCTCCCGAGCG
CCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGCGGTCGAGTGAAC
ACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCTTCGCCAAGTTCATCTAGGGTCTG
CTGG

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSWGGLIHLYTATARNSYHLQIHKNGHVD
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLENGY
DVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQLSRNEIPLIHFNTPIPRRHTRSAEDDSE
RDPLNLVLKPRARMTAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTGPEGCRPFA
KFI

Important features of the protein:**Signal peptide:**

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

GGAAGAGGTACCCGAGAGACAGCCAGGTTCTGTGGAGACAGCGGTGCCCGGCTAGG**ATC**
 GGCTGTCTCTGGGGTCTGGCTCTGCCCTTTTCTTCTTCTGCTGGGAGGTTGGGGTCTCTGG
 GAGCTCTGCAGGCCCCAGCACCCGAGAGCAGACACTGCGATGACAAACGGACGACACAGAAG
 TGCCCGCTATGACTCTAGCACCGGGCCACGCCGCTCTGGAAACTCAAACGCTGAGCGCTGAG
 ACCTCTTCTAGGGCTCAACCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGCCAA
 GAGAAATTTCCCTGCAAGAGAGACCAGGAGTTTCAAAAACATCTCCAACTTCATGTGTC
 TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
 ACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCTTTGCACCCGA
 TGACAGCTCTGAAGAGGCAAAGACACTCACAAATGGACATATTGACATTGGCTCACACCTCCA
 CAGAAGCTAAGGGCCTGTCTCAGAGAGCAGTGCTCTTCCGACGGCCCCCATCCAGTCATC
 ACCCCGTCACGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATACCCCC
 GTCACGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATACCCCCGTCAT
 GGTCCCCGGGATCTGATGTCACTCTCTCTGCTGAAGCCCTGGTGACTGTCAAAACATCGAG
 GTTATTAAATTGACGATCACAGAAATAGAAACAACAATCTCCAGCATCCCTGGGGCTCAGA
 CTATAGATTCATCCCCACGGAAGGGGTGAAGCGCTCTGCCATCCGATCCACCGACTCTGC
 CTGACTCCACTGAAGCAAACCACATCACTGAGGTACAGCCTCTGCCGAGACCGCTGTCC
 ACAGCCGGCACCCAGAGTCACTGCACCTCATGCCACGGTTGGGAGCCCCATCCCCACTAA
 CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGCCACGACCCCTCAGTGGAGCTCTGGTCA
 CAGTTAGCAGGAATCCCTGGGAAGAACTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC
 AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTGAGCAGTGGGCAAAAACAATT
 CTTTGTCTGGGAGCTCTGCTTCTCTACAGCCCTCGGAAGCCGCCCTCAAGAACTTCACCC
 CTTCAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCACCAGCAGGGACCCT
 CTTCTCTCTGTCTCTCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
 GATCACAACTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCACGACTGCCCGGAC
 GAGGCCGACCACAGAGCT**GTA**GTGCAGGTGAAATGAGAGTTTCTCTCTCTGCGGCTGAGTG
 TGGCTTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
 CGGGAACCTCCACGCCACGCGCTCACTTCCAGGTCTCCTTACTGCGTGTCAAGGAGGGCTA
 ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGTGCCCTTAGCCTG
 GGCCCCCACCAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
 AAGGGCAGCATGTCCAAGCCCTAACCCAGATGTGGCAACAGGACCCCTCGCTCACATCCAC
 CGGAGTGTATGTGTGGGAGGGGCTTACCTGTTCCAGAGGTGTCTTGGACTACCTTGG
 CAGATGTTCTGTGTTTCAGTAAGAGAGACCTGATCACCATCTGTGTGCTTCCATCCTGCA
 TTAAATTCACCTCAGTGTGGCCGAAAAAAA

FIGURE 326

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTL
 ETSSRASTPAGPIPEAETRGAKRISPARETRSF TKTS PNFMVLIATSVETSAASGSPEGAGM
 TTVQITITGSDPEEAIFD TLCTDDSS EEA KTLTMDILT LAHTSTEAKGLSS EESSASSD GPHPV
 ITPSRASESSASSD GPHPVITPSRASESSASSD GPHPVITPSWSPGSDVTL LAEALVTVTNI
 EVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL
 STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTL SGALVTVSRNPLEETSALS VETPSY
 VKVSGAAPVSI EAGSAVGKTTSFAGSSASSYSPSEAALKNF TPSETPTMDIATKGFPPTSRD
 PLPSVPPTTTNSSRG TNSTLAKITTS AKTTMKPQQPRRLPGRGRPQT

N-glycosylation sites:

amino acids 252-256, 445-449, 451-455

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-90

Casein kinase II phosphorylation sites.

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
 404-408, 414-418, 431-435

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-
 320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 327

GCGGAGCATCCGCTGCGGTCTCGCCGAGACCCCGCGGGATTGCGCGGTCTTCCGCGG
 GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGCGCGGGGTCTCTCGACGCCA
 GAGAGAAATCTCATCTGTGCAGCCTTCTTAAAGCAAACCTAAGACCAGAGGGAGGATTAT
 CCTTGACCTTTGAAGACCAAACTAACTGAAATTTAAAAATGTTCTTCGGGGGAGAAGGGAG
 CTTGACTTACACTTTGGTAATAATTTGCTTCTGACACTAAGGCTGTCTGTAGTCAGAATT
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCTATTGACATCCAGTCATCTCTTTCTAAGGGAATC
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATCTTGTCTGTTCAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACTTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCCAACCTGCTACCTATTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCA
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
 CCAAGAGTTACCCAGGAAGATTCTCTCTTACATGGCCAATTTTCAACAGCAGTCACCTCCC
 TAGCCCATCATCACACAGATTATTTCAAAGCCCAACCGATATCTCATGGAGAGACACACTTTCT
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTAAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAAATTTTCTCTGATCAAGAAA
 TAGCTCATCTGCTGCCTGAAATGTGAGTGCCTCCAGCTACGGTGCCAGTTGCTTCTCCA
 CATACCACCTCGGCTACTCCAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACC
 TTTCTGGGACTTCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAAACCACTGTCACTTCTC
 AGCCTCCCACGACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG
 GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA
 AACCATACCGTTTACAGAAATCTCCAACCTAACTTTGAACACAGGGAATGTGTATAACCCCTA
 CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTCTGGGAAGGT
 AGGGAGGCCAGTCCAGGCAGTTCTCTCCAGGGCAGTGTTCCAGAAAAATCAGTACGGCCTTCC
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGCTCGTTCCTGGTGATAGGCC
 TCGTCTCTCTGGGTAGAATCCTTTCGGAATCACTCCGACAGAAACGTTACTCAAGACTGGAT
 TATTTGATCAATGGGATCTATGTGGACATCTAAAGGATGGAACCTCGGTGCTCTTAATTCATT
 TAGTAACCAAGACCCCAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTG
 TATTTTGAAGACAGGAAATGCCCCCTTCTGCTTCTCTTTTTTTTTTGGAGACAGAGTCTT
 GCTCTGTTGCCAGGCTGGAGTGCAAGTACACGATCTCGGCTCTCACCGCAACCTCCGTCTC
 CTGGGTTCAAGCGATTCTCCTGCCTCAGCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACCTGGGTGATTTTGTATTTTGTAGTAGACGGGTTTCAACATGTTGGTCAGGCTG
 GTCTCAAACCTCTGACCTAGTGATCCACCTCCTCGGCTCCCAAGTGTCTGGGATTACAGG
 CATGAGCCACACAGCTGGCCCCCTTCTGTTTATGTTTGGTTTTTGAAGGAATGAAGTG
 GGAACCAAAATTAGGTAATTTTGGGTAATCTGTCTCTAAATATAGCTAAAAACAAGCTCT
 ATGTAAAGTAATAAGTATAATTGCCATATAAATTTCAAATTCAACTGGCTTTTATGCAAA
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATTCACATCTTGGTTCAGATAAAATCAAC
 TGTTTATACAAATTTCTAATGGATTGCTTTTCTTTTATATGGAATCCCTTTAAAACTTAT
 CCAGATGTAGTTCTTCCAATTAATATTTGAATAAATCTTTTGTACTCAA

FIGURE 328

>>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGSLTYTLVIICFLTTLRLSASQNCCLKSLEDVVIDIQSSLSKGIRGNEPVYTTQED
CINSCCSTKNISGDKACNLMIFDTRKTRARQPCYLFPCNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEIHAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTFPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFEEKWLLIGSLFLGVLFLVIGLVLLGRILSES LRKRYSRLDYLINGIYVDI

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 329

CTCCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCTGCTATGGGGTGGCTGCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCAAGGGGACACTGTGT
 CCTTGCAGTGCACCTACAGGGAAGAGCTGAGGGACACCAGGAAGTACTGGTGCAGGAAGGGT
 GGCATCCTCTTCTCTCGTGCTCTGGCACCATCTATGCAGAAGAAGGAGGAGACAAAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTACCCCTGTGGA
 ACCTCACCCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG
 TCTTTTACTGATCTCTCTGTTCGTCTTTCCAGGACCCTGCTGTCCTCCCTCCCCCTTCTCCAC
 CTTCCAGCCTCTGGCTACAACACGCCCTGCAGCCCAAGGCAAAAGCTCAGCAAACCCAGCCCC
 CAGGATTGACTTCTCTGGGCTCTACCCGGCAGCCACAGCCAAGCAGGGGGAAGACAGGG
 GCTGAGGCCCTTCAATTGCCAGGGACTTCCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCCTCACCAGCGACCTCTCCTCCTGCAGGGAGCTCCCGCCCCCATGTCAGC
 TGGACTCCACCTCAGCAGAGGACACCACTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCAGG
 GTGTCCATCCCAGTGGTCCGCATATCGGCCCCAGTCTGTGGTCTGCTGAGCCTTCTGTTCAGC
 CGCAGGGCTGATCGCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA
 CGGAGTACAGAGGAAGACGAGAAGTTCTGGCTCTCAGCCTTGACTCGCGAGGAAAGGAAGCC
 CCTTCCAGGGCCCCTGAGGGGGACGTGATCTCGATGCCTCCCTCCACACATCTGAGGAGGA
 GCTGGGCTTCTCGAAGTTTGTCTCAGCGTTAGGGCAGGAGGCCCTCTGGCCAGGCCAGCAGT
 GAAGCAGTATGGCTGGGTGATCAGCAGCCGATTCCGAAAGCTTCCACCTCAGCCCTCAGAG
 TCCAGCTGCCCGGACTCCAGGGCTCTCCCCACCTCCCCAGGCTCTCCTCTGGCATGTGTCCA
 CGCTGACCTAGAAGGCTTTGTAGCCCTGGAGCCACAGCGTGGCCCTTGCTCTTCCGGCTG
 GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGC
 CTATGCCCCAGTGTGCGGACCCTGCCTTCCCTCCACTCCAGACCCCCACCTTGCTTCCCTCCC
 TGGCGTCTCAGACTAGTCTCCACGGTCTCCTGTCATCAGCTGGTGATGAAGAGGAGCATGCT
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACTGCATCCAGCCTTCAAGAACCT
 GTGAAAAACGTGATTCTCTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG
 GACTCTGAATTCTAACAATGCCAGTACTGTGCACTTGAGTTTGAAGGCCAGTGGGCCCTG
 ATGAACGCTCACACCCTTTCAGCTTAGAGTCTGCATTGGGCTGTGACGTCTCCACCTGCC
 CAATAGATCTGCTCTGCTGCGACACCAGATCCACGTGGGACTCCCTGAGGCCTGCTAAG
 TCCAGGCCTTGGTCAGGTCAGGTGCACATTGCAGGATAAGCCAGGACCGGCACAGAAGTGG
 TTGCCTTTNCCATTTCGCCCTCCCTGNNCCATGCCCTTCTGGCTTTGGAAAAAATGATGAAGA
 AAACTTGGCTCCTTCTTGTCTGGAAGGGTTACTTGCCATTGGGTTCTGGTGGCTAGAGA
 GAAAAGTAGAAAAACAGAGTGCACGTAGGTGTCTAACACAGAGGAGTAGGAACAGGGCGG
 ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTGCGGGGTGGTGGTAAAGTA
 GCACAATCTACTATTTTTTTTCTTTTTCCATTATATTTGTTTTTAAAGACAGAATCTCGTGCT
 GCTGCCAGGCTGGAGTGCAGTGGCACGATCTGCAAACTCCGCCCTCCTGGGTTCAAGTGATT
 CTCTGCTCAGCTCCCGAGTAGCTGGGATTACAGGCACGCACCACCACCTGGCTAATT
 TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTGGCCAGGCTGGTCTTGAACCTCTGAC
 CTCAAATGAGCCTCCTGCTCTCAGTCTCCCAAAATGGCGGATTACAGGCATGAGCCACTGTG
 TCTGGCCCTATTTCTTTAAAAAGTGAATTAAGAGTGTGTCAGTATGCAAACTTGGAAAG
 ATGGAGGAAAAAGAAAGGAGAAAAAATGTCAACCATGCTACCCAGACTCACCAGACATCAT
 TATTTCTGTTTTGTTGTAATCTTCTTCCACTCTTTCTTCTTACATAATTTGCCGGTGTCTTT
 TTTACAGAGAATATCTGTATATACAACCTTGTATCCTGCCTTTTCCACCTTATCGTTCC
 ATCATTATTTACGACTTCTCTGTGTTTACAGACCTTTTATAAATAAATGTTCTATCA
 GCTGCATAAAAAAAAAAAAAA

FIGURE 330

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALGPEEISGFEGD TVSLQCTYREELRDHRKYWCRKGGILFSRCS
GTIYAE EEGQETMKG RVSI RDSRQELSLIVTLWNLTLDAGEYD WCGVEKRGFPDESLLISLFV
FPGPCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEPPLPG
TSQYGHERTSQYTGTSHPHPATSPFAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLRKEAQQATETQRNEKFWLSRLTAEKEAPSQAPEGD
VISMPPLHTSEEELGFSKFVSA

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128